

STIC-Biotech/ChemLib

96753

From: McGarry, Sean  
Sent: Tuesday, June 17, 2003 10:12 AM  
To: STIC-Biotech/ChemLib  
Subject: SEQ SEARCH 09/964,666

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JUN 17 2003

(STIC)

Sean McGarry 73484  
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CM1 11E12 Mailbox  
305-7028

09/964,666

Please, a length limited (nt  $\leq$  50) search of SEQ ID NOS 9-14.

Thank You

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 6/17/03  
Date Completed: 6/23/03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: 10  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: 01  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 522.031 Seconds

(without alignments)  
1449.478 Million cell updates/sec

Title: US-09-964-666-10

Perfect score: 26

Sequence: 1 TGTGTCATGCTTGTGTCACAGCTAC 26

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_ov:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_ro:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_un:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_hlg\_mus:\*  
34: em\_hlg\_din:\*  
35: em\_hlg\_fod:\*  
36: em\_hlg\_mam:\*  
37: em\_hlg\_vrt:\*  
38: em\_sy:\*  
39: em\_hlg\_hum:\*  
40: em\_hlg\_mus:\*  
41: em\_hlg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.2	62.3	21	6	AX050293 Sequence
2	16	61.5	50	6	AX199678 Sequence
3	15.6	60.0	47	6	AX378267 Sequence
4	15.2	58.5	20	6	AR067246 Sequence
5	15.2	58.5	21	6	AX117706 Sequence
6	15.2	58.5	27	6	AX429427 Sequence
7	15	57.7	27	6	AX116084 Sequence
8	15	57.7	28	6	AR164904 Sequence
9	15	57.7	44	6	AR116815 Sequence
10	14.8	56.9	36	6	AR023949 Sequence
11	14.8	56.9	36	6	II12127 Sequence
12	14.8	56.9	36	6	II15450 Sequence
13	14.8	56.9	36	6	II1297 Sequence
14	14.4	55.4	20	6	I31358 Sequence
15	14.4	55.4	41	6	I32222 Sequence
16	14.2	54.6	19	6	AX010420 Sequence
17	14.2	54.6	42	6	AR022354 Sequence
18	14	53.8	31	6	AX248371 Sequence
19	14	53.8	31	6	AX249312 Sequence
20	14	53.8	33	6	AX405134 Sequence
21	14	53.8	37	6	AX477864 Sequence
22	14	53.8	45	9	HS4224254 Sequence
23	13.8	53.1	34	6	AX184141 Sequence
24	13.8	53.1	37	6	AX040679 Sequence
25	13.8	53.1	42	6	AX173376 Sequence
26	13.6	52.3	24	6	AX291119 Sequence
27	13.6	52.3	31	6	AX249648 Sequence
28	13.6	52.3	38	6	AR078070 Sequence
29	13.6	52.3	38	6	E35651 Sequence
30	13.6	52.3	39	6	AR078068 Sequence
31	13.6	52.3	39	6	AR098737 Sequence
32	13.6	52.3	39	6	E35649 Sequence
33	13.6	52.3	39	6	E35696 Sequence
34	13.4	51.5	17	6	AR171891 Sequence
35	13.4	51.5	21	6	AR169512 Sequence
36	13.4	51.5	25	6	AX476156 Sequence
37	13.4	51.5	25	6	AX476157 Sequence
38	13.4	51.5	25	6	AX476158 Sequence
39	13.4	51.5	30	6	I89866 Sequence
40	13.4	51.5	31	6	BD002550 Gene comp
41	13.4	51.5	32	6	AX234354 Sequence
42	13.4	51.5	35	6	AR040575 Sequence
43	13.4	51.5	35	6	AR055599 Sequence
44	13.4	51.5	37	6	AX223015 Sequence
45	13.4	51.5	39	6	AR040576 Sequence

## ALIGNMENTS

RESULT 1  
LOCUS AX050293 21 bp DNA  
DEFINITION Sequence 47 from Patent WO0070046.  
ACCESSION AX050293  
VERSION AX050293.1 GI:12226574  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Shimkets,R.A., Fernandes,E. and Boldog,F.  
TITLE Secreted polypeptides and corresponding polynucleotides  
JOURNAL Patent: WO 0070046-A 47 23-NOV-2000;  
Curagen Corporation (US)

	FEATURES	Location/Qualifiers 1..21
	SOURCE	/organism="synthetic_construct" /db_xref="taxon:32630" /note="Chemically synthesized"
	BASE COUNT	4 a      7 c      5 g      5 t
	ORIGIN	
OY	Query Match	62.3%; Score 16.2; DB 6;
	Best Local Similarity	85.7% Pred. No. 1.2e+04;
Matches	18; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Db	5 GCATGCTTTTGTCACACTA 25	
	1 GCATGCCGTAGTCCCACTA 21	
RESULT 2	AXI99678/c	50 bp DNA linear PAT 29-AUG-2001
LOCUS	AXI99678	
DEFINITION	Sequence 608 from Patent WO0151670.	
ACCESSION	AXI99678	
VERSION	AXI99678.1 GI:15390118	
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 50)	
REFERENCE	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof	
AUTHORS	Patent: WO 0151670-A 608 19-JUL-2001;	
TITLE	Curagen Corporation (US) Location/Qualifiers	
JOURNAL	1..50	
FEATURES	/organism="Homo sapiens" /db_xref="taxon:3606"	
SOURCE	25..26	
	/note="Nucleotide deleted between bases 25 and 26	
	Accession number cg44129408"	
misc-feature	26	
	/note="2 of 2 allelic variants (607 is other entry)"	
BASE COUNT	14 a    12 c    11 g    13 t	
ORIGIN		
Query Match	61.5%; Score 16; DB 6; Length 50;	
Best Local Similarity	79.2%; Pred. No. 1.4e+04;	
Matches	19; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
OY	3 GTGCATGCTTTGGTCCCAGCTAC 26	
Db	26 GCCCATCGCCTGAATCCAGCTAC 3	
RESULT 3	AXJ78267/c	47 bp DNA linear PAT 18-MAR-2002
LOCUS	AXJ78267	
DEFINITION	Sequence 56 from Patent WO0206525.	
ACCESSION	AXJ78267	
VERSION	AXJ78267.1 GI:19574117	
KEYWORDS		
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 56)	
REFERENCE	Cohen,D., Blumenfeld,M., Chuinakov,I., Abderrahim,H. and Bihain,B. Obesity associated diallelic marker maps	
AUTHORS	Patent: WO 0206525-A 56 24-JUN-2002;	
TITLE	GENSER (FR)	
JOURNAL	Location/Qualifiers	
FEATURES	1..47	
SOURCE		

		/organism="Homo sapiens"	
variation		/db_xref="taxon:9606"	
		24	
		/note="99-27232-379 : polymorphic base A or G"	
BASE COUNT	9 a	20 c	10 g
ORIGIN	7 t 1 others		
Query Match 60.0%; Score 15.6; DB 6; Length 47;			
Best Local Similarity 75.0%; Pred. No. 2.2e+04;			
Matches	18; Conservative	1; Mismatches	5; Indels 0; Gaps 0;
Oy	1 TGGTCATGCTTTGGTCCAGCT 24		
	1       1		
Db	40 TAGTCATGCTTACAGTCCAGCT 17		
RESULT 4			
LOCUS	AR067246	20 bp	DNA
DEFINITION	Sequence 594 from patent US 5851760.		
ACCESSION	AR067246		
VERSION	AR067246.1	GI:5998468	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 20)		
TITLE	Evans, G.A. and Smith, M.W.		
JOURNAL	Method for generation of sequence sampled maps of complex genomes		
FEATURES	Patent: US 5851760-A 594 22-DEC-1998;		
	Location/Qualifiers		
	1..20		
BASE COUNT	5 a	3 c	9 g
ORIGIN	3 t		
Query Match 58.5%; Score 15.2; DB 6; Length 20;			
Best Local Similarity 85.0%; Pred. No. 3.7e+04;			
Matches	17; Conservative	0; Mismatches	3; Indels 0; Gaps 0;
Oy	7 ATGCTTTGGTCCAGCTAC 26		
	1		
Db	20 ATCCCTGTGTCACAGCTAC 1		
RESULT 5			
LOCUS	AX117706	21 bp	DNA
DEFINITION	Sequence 2829 from Patent W00129262.		
ACCESSION	AX117706		
VERSION	AX117706.1	GI:14034657	
KEYWORDS			
SOURCE	Synthetic construct.		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 21)		
AUTHORS	Picolet-Newburg, L. and Pohl, M.		
TITLE	Genotyping reagents, kits and methods of use thereof		
JOURNAL	Patent: WO 0129262-A 2829 26-APR-2001;		
FEATURES	Orchid Biosciences, Inc. (US)		
	Location/Qualifiers		
	1..21		
BASE COUNT	5 a	4 c	7 g
ORIGIN	5 t		
Query Match 58.5%; Score 15.2; DB 6; Length 21;			
Best Local Similarity 85.0%; Pred. No. 3.7e+04;			
Matches	17; Conservative	0; Mismatches	3; Indels 0; Gaps 0;
Oy	7 ATGCTTTGGTCCAGCTAC 26		







BASE COUNT                      /organism="unknown"  
ORIGIN                      4 a                      12 c                      14 g                      11 t

Query Match                      55.48;                      Score 14.4;                      DB 6;                      Length 41;  
Best Local Similarity                      75.08;                      Pred. No. 8e+04;  
Matches 18;                      Conservative 0;                      Mismatches 6;                      Indels 0;                      Gaps 0;

OY                      3 GTGCATGCTTGGTCCAGCTAC 26  
                    |||| | | | | | | | | | |  
Db                      7 GTCCGAGGCTGTGGGCCCACTAC 30

Search completed: June 21, 2003, 22:14:28  
Job time : 527.031 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:51 ; Search time 142.594 Seconds  
(without alignments)  
410.621 Million cell updates/sec

Title: US-09-964-666-10

Sequence: 1 TGTGTCATGCTTTGTGCCACACTAC 26

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq\_101002:\*

1: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*

2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*

3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*

4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*

5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*

6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*

7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*

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13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*

14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*

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16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*

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19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*

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22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*

23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*

24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.6	67.7	31	20	AA06149
2	17.2	66.2	33	24	ABL40961
3	16.2	62.3	21	22	AA23445
4	16	61.5	50	22	AA89827
5	15.6	60.0	47	24	ABK40808
6	15.2	58.5	20	16	AA082594
7	15.2	58.5	21	22	AAH4003
8	15.2	58.5	27	24	ABK92971
9	15.2	58.5	36	21	AAA35578

C	10	15.2	58.5	50	22	AA131378	Human SNP oligonuc
C	11	15	57.7	27	22	AA838411	SNP specific SNPE
C	12	15	57.7	28	21	AA292014	Mahogany protein 9
C	13	15	57.7	44	20	AA36190	Intronic location
C	14	15	57.7	40	22	AA29684	Human SNP oligonuc
C	15	14.8	56.9	41	24	ABN87593	Oligodendrocyte-my
C	16	14.4	55.4	20	18	AA65953	Primer #2 to amplif
C	17	14.4	55.4	31	22	AA129962	Human single nucle
C	18	14.4	55.4	31	22	AA130903	Human single nucle
C	19	14.4	55.4	41	16	AA091982	FSH-beta probe
C	20	14.2	54.6	19	21	AA45351	Sense PCR primer u
C	21	14.2	54.6	19	21	AA239844	PCR primer 1 for t
C	22	14.2	54.6	20	20	AA90795	Human 7SL RNA spec
C	23	14.2	54.6	41	24	ABL40963	Transcription regu
C	24	14.2	54.6	41	24	ABL40964	Transcription regu
C	25	14.2	54.6	42	24	AB862843	Human protective D
C	26	14.2	54.6	48	24	AB862842	Human protective D
C	27	14.2	54.6	50	19	AAV32917	Aspergillus niger
C	28	14	53.8	33	22	AA165991	Human protein asso
C	29	14	53.8	33	24	AA039460	Maize PPDK cDNA am
C	30	14	53.8	37	24	ABN89108	Human prostate spe
C	31	14	53.8	48	24	ABN72411	Streptococcus agal
C	32	13.8	53.1	34	22	AAH91368	Human inflammatory
C	33	13.8	53.1	37	21	AA668148	Cystatin mutagenic
C	34	13.8	53.1	42	22	AA506929	Forward PCR primer
C	35	13.8	53.1	50	22	AA130574	Human SNP oligonuc
C	36	13.6	52.3	24	24	AB188158	Capture oligonucle
C	37	13.6	52.3	25	21	AA87504	Capture oligonucle
C	38	13.6	52.3	25	21	AA427304	Fas ligand promote
C	39	13.6	52.3	25	22	AA421322	Human MDR-1 allele
C	40	13.6	52.3	33	22	AAH84200	Human cell death p
C	41	13.6	52.3	38	20	AA56332	Neisseria gonorrhoe
C	42	13.6	52.3	39	20	AA56330	Neisseria gonorrhoe
C	43	13.6	52.3	39	20	AA30271	Neisseria gonorrhoe
C	44	13.6	52.3	50	22	AA129143	Human SNP oligonuc
C	45	13.4	51.5	17	20	AA84625	PCR primer for Hum

# ALIGNMENTS

RESULT 1  
AA06149/c  
ID AA06149 standard; DNA; 31 BP.

AC AA06149;

XX

XX 31-MAR-1999 (first entry)

XX

DE Human biallelic polymorphic DNA fragment WI-17197.

XX

KW Polymorphism: biallelic; paternity testing; forensic; genetic mapping;

KW phenotypic typing; medicament; disease; marker; human; ss.

XX

OS Homo sapiens.

XX

PN W09858529-A2.

XX

PD 30-DEC-1998.

XX

XX 22-JUN-1998; 98WO-US12930.

XX

XX 24-JUN-1997; 97US-0050594.

XX

PA (AFFY-) AFFYMETRIX INC.

XX

PI Beruo A, Chee M, Fan J, Lipshutz RJ;

XX

DR WPI; 1999-080963/07.

XX

PT New nucleic acid segments containing polymorphic sites - used for,

PT e.g. detecting a disease phenotype, in forensics, paternity testing

PT or genetic mapping of phenotypic traits



CC inhibit thromboses, infections caused by bacteria, virus, fungi and other  
 CC parasites, and as a vaccine. SECX antibodies may be used to isolate or  
 CC detect SECX proteins, monitor protein level in tissue as part of a  
 CC clinical testing procedure, treat proliferative disorders including  
 CC tumours and benign hyperplasias.

XX Sequence 21 BP; 4 A; 7 C; 5 G; 5 T; 0 other;

Query Match 62.3%; Score 16.2; DB 22; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 4.8e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 GCATGCTTTGGTCCAGCTA 25  
 1 GCATGCCCTGATGCCAGCTA 21

#### RESULT 4

AAH89827/c standard; DNA: 50 BP.

XX AAH89827;

XX 01-OCT-2001 (first entry)

DE Human coding sequence polymorphic site SEQ ID NO: 608.

XX Human: single nucleotide polymorphism: SNP: paternity test;  
 KW forensic test; aberrant protein expression; ds.

XX Homo sapiens.

XX MO200151670-A2.

XX 19-JUL-2001.

XX 05-JAN-2001; 2001MO-US00322.

XX 07-JAN-2000; 2000US-0174962.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2001-451871/48.

XX P-PSDB; AAM00708.

PT Isolated human polynucleotides containing single nucleotide  
 PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,  
 PT infection and diabetes -

XX Claim 1; Page 279; 475pp; English.

CC The present invention relates to human nucleic acids containing single  
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and  
 CC paternity tests, and to aid in the treatment of diseases associated with  
 CC aberrant protein expression, including cancer, amyloidosis, diabetes,  
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,  
 CC glomerulonephritis, hemolytic anaemia, thrombocytopaenia, arthritis,  
 CC meningitis, muscular disorders, dementia, neurological diseases, tubercous  
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or  
 CC autoimmunity. The present sequence is a polymorphism-containing  
 CC oligonucleotide fragment of the invention.

XX Sequence 50 BP; 14 A; 12 C; 11 G; 13 T; 0 other;

Query Match 61.5%; Score 16; DB 22; Length 50;  
 Best Local Similarity 79.2%; Pred. No. 6.7e+02;  
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 GTGATGCTTTGGTCCAGCTAC 26  
 1 TTTTTT T T TTTTTTTTTT

Db 26 GCCATGCCCTGATGCCAGCTAC 3

#### RESULT 5

ABK40808/c standard; DNA: 47 BP.

XX ABK40808;

XX 21-MAY-2002 (first entry)

DE Human obesity-associated chromosome 10 biallelic marker #40.

XX Human: obesity associated biallelic marker; chromosome 10; obesity; ds;  
 KW drug response; hyperuricaemia; digestive pathology; hypertension; cancer;  
 KW hepatic function disorder; cardiovascular disease; hyperlipidemia;  
 KW insulin disorder; atheromatous disease; cardiac insufficiency.

XX Homo sapiens.

XX MO200206525-A2.

XX 24-JAN-2002.

XX 28-JUN-2001; 2001MO-IB01477.

XX 18-JUL-2000; 2000US-219704P.

XX (GEST ) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I, Abderrahim H, Blhain B;

XX WPI; 2002-155043/20.

PT Set of novel map-related biallelic markers, preferably located on  
 PT obesity disorder-associated chromosomal regions on chromosomes 3, 10  
 PT and 19, useful, for e.g. detecting statistical correlations between  
 PT marker allele and a phenotype -

XX Claim 1; Page 203; 311pp; English.

CC The invention relates to a set of novel map-related biallelic markers,  
 CC preferably located on obesity disorder-associated chromosomal regions on  
 CC chromosomes 3, 10 and 19. The markers are useful for genotyping or  
 CC estimating the frequency of an allele in a population, for detecting an  
 CC association between a genotype or haplotype and a phenotype, e.g. a  
 CC disease involving drug responses, obesity or disorders related to  
 CC obesity, such as hyperuricaemia, digestive pathology, hepatic function  
 CC disorders, cancer, cardiovascular disease, hypertension, hyperlipidemia,  
 CC insulin disorders, atheromatous disease and cardiac insufficiency. The  
 CC markers are useful for detecting a statistical correlation between a  
 CC biallelic marker allele and a phenotype and/or between a biallelic marker  
 CC haplotype and a phenotype. This sequence represents a human  
 CC obesity-associated biallelic marker located on chromosome 10.

XX Sequence 47 BP; 9 A; 20 C; 10 G; 7 T; 1 other;

Query Match 60.0%; Score 15.6; DB 24; Length 47;  
 Best Local Similarity 75.0%; Pred. No. 1e+03;  
 Matches 18; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 TGGTGCATGCTTTGGTCCAGCT 24  
 1 TTTTTT T T TTTTTTTTTT  
 Db 40 TAGTGCATGCCCTACAGTCCAGCT 17

#### RESULT 6

AAO82594/c standard; DNA: 20 BP.

XX AAO82594;

XX 14-SEP-1995 (first entry)

```

XX DE Chromosome 11 (Locus D11S863) STS primer MS20-2.
XX XX
XX KW sequence sampled mapping; genomic analysis; complex genome mapping;
XX KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX OS Synthetic.
XX PN MO9429486-A.
XX PD 22-DEC-1994.
XX PE 15-JUN-1994; 94WO-US06810.
XX PR 15-JUN-1993; 93US-0078471.
XX PR 07-SEP-1993; 93US-011952.
XX PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX PI Evans GA, Smith MW;
XX DR WPI; 1995-036508/05.
XX PT Sequencing complex genomes, present as fragments in a cosmid
XX PT library - by sequencing end-specific nucleotides of each clone
XX PT then correlating with spatial relationship of cosmid, esp. for
XX PT mammalian chromosomes.
XX PS Example 4; Page 89; 128bp; English.
XX XX
XX CC Sequences were determined from the ends of chromosome 11-specific
XX CC cosmid by automated sequencing without intermediate subcloning.
XX CC A sample of 371 DNA sequence fragments were determined and of
XX CC these, 277 were suitable for STS primer prediction by computer.
XX CC CC analysis (using the "primer" program available from F.Lander, MIT).
XX CC The STSs and cosmids were mapped by in situ hybridization, somatic
XX CC cell hybrid analysis or both. Using this method, 370 STSs specific
XX CC for human chromosome 11 were generated and most of them were
XX CC regionally mapped. This procedure illustrates a novel method for
XX CC sequencing complex genomes, designated "sequence sampled mapping".
XX CC CC The sequence sampled mapping method is useful for the completion of
XX CC high density sequence-based maps, and ultimately for the complete
XX CC sequencing of genomic DNA directly from cosmid clones.
XX CC See AAQ82001-Q82706 and AAQ91325-Q91358 for STS primers.
XX SQ Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 other;
XX XX
XX Query Match 58.5%; Score 15.2; DB 16; Length 20;
XX Best Local Similarity 85.0%; Pred. NO. 1.4e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 ATGCTTTGGTCCAGCTAC 26
DB 20 ATCCCTGTGCTCCAGCTAC 1

```

```

RESULT 7
AAH40033/c
ID AAH40033 standard; DNA: 21 BP.
XX
XX AAH40033;

```

```

XX DE 14-AUG-2001 (first entry)
XX SNR specific upper PCR primer SEQ ID 2829.
XX
XX

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XX KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX KW SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
XX KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX

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OS Homo sapiens.
XX
XX PN MO200129262-A2.
XX PD 26-APR-2001.
XX PF 13-OCT-2000; 2000MO-US28436.
XX PR 15-OCT-1999; 99US-0160096.
XX PA (ORCH-) ORCHID BIOSCIENCES INC.
XX PI Picoult-Newburg L, Pohl M;
XX DR WPI; 2001-290930/30.
XX PT New genotyping oligonucleotide, useful for detecting the presence,
XX PT absence or identity of single polynucleotide polymorphism in a nucleic
XX PT acid sample
XX PS Claim 1; Page 64; 83pp; English.
XX XX
XX CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX CC primer extension (SNPE) primers, and the sequences of regions flanking
XX CC sites of single nucleotide polymorphisms SNPs. The present invention
XX CC includes kits for determining the presence or absence of a SNP, using the
XX CC oligonucleotides of the invention. The PCR primers are used to amplify a
XX CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
XX CC The oligonucleotides are useful for genotyping a nucleic acid sample by
XX CC performing a single-nucleotide primer extension reaction. The
XX CC oligonucleotides are useful for determining the presence, absence or
XX CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX CC assess by association analysis the genotype of an individual or group of
XX CC individuals, having a pathological phenotypic trait suspected of being
XX CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
XX CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX CC traits also include symptoms of or susceptibility to multifactorial
XX CC diseases of which a component is or may be genetic such as autoimmune
XX CC diseases, including, rheumatoid arthritis, multiple sclerosis,
XX CC inflammation, cancer, nervous system diseases and infection by pathogenic
XX CC microorganism. The method is also useful in forensic investigations and
XX CC paternity analysis. The present sequence represents a PCR primer specific
XX CC for a human SNP containing DNA sequence.
XX SQ Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 other;
XX XX

```

```

XX Query Match 58.5%; Score 15.2; DB 22; Length 21;
XX Best Local Similarity 85.0%; Pred. NO. 1.4e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 ATGCTTTGGTCCAGCTAC 26
DB 21 ATGCTGTAGTCCAGCTAC 2

```

```

RESULT 8
ABK92971
ID ABK92971 standard; DNA: 27 BP.
XX
XX ABK92971;

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XX DE 22-AUG-2002 (first entry)
XX
XX

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XX KW Genomic analysis method PCR primer 3'DEGIS431.
XX KW Genomic analysis; PCR; primer; ss.
XX OS Synthetic.
XX PN MO200234939-A2.
XX

```



PD 02-MAY-2002.  
 XX 22-OCT-2001; 2001WO-CA01487.  
 PF 23-OCT-2000; 2000US-0695545.  
 XX (MBIF-) MBI FERMENTAS INC.  
 PA Yu AHC;  
 PI WPI; 2002-489951/52.  
 DR  
 XX Analysing a DNA sample, involves using an extension primer generated by  
 PT capturing unknown DNA with an adaptor containing a class IIS  
 PT restriction enzyme recognition site in an extension/amplification  
 PT reaction with DNA sample -  
 XX  
 PS Example 1; Page 21; 79pp; English.  
 CC The invention describes a method of analysing a DNA sample using  
 CC ligation, digestion and extension techniques. The method is also  
 CC useful for identification and analysis of unknown sequences upstream  
 CC of a known region or sequence. This sequence represents a PCR primer  
 CC used in analysis of sequences captured from a restriction endonuclease  
 CC digest of bacterial genomic DNA.  
 CC  
 SQ Sequence 27 BP; 6 A; 6 C; 4 G; 8 T; 3 other;  
 Query Match 58.5%; Score 15.2; DB 24; Length 27;  
 Best Local Similarity 68.0%; Pred. No. 1.4e+03;  
 Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 OY 1 TGGTCATGCTTTGGTCCACGCTA 25  
 1 TGGTCATGCTTTGGTCCACGCTA 25  
 DB 1 TGGTCATGCTTTGGTCCACGCTA 25  
 RESULT 9  
 AAA35578  
 ID AAA35578 standard; DNA; 36 BP.  
 XX  
 AC AAA35578;  
 XX  
 DT 26-JUL-2000 (first entry)  
 XX  
 DE Permutin linker encoding nucleotide sequence FG33.  
 XX  
 KW Biologically-activated circularly-permuted protein; permutin; linker;  
 KW permutin library generation; therapeutic property; antigen;  
 KW immunotherapy; improve bio-distribution; half life; ss.  
 XX  
 OS Synthetic.  
 XX  
 KW WO200018905-A1.  
 PN  
 XX  
 OS 06-APR-2000.  
 PD  
 XX 24-SEP-1999; 99WO-US20891.  
 PF  
 XX 25-SEP-1998; 98US-0101908.  
 PR  
 XX (SEAR ) SEARLE & CO G D.  
 PA  
 PI Lee SC;  
 XX  
 DR WPI; 2000-293145/25.  
 XX  
 PT Preparation of biologically-activated circularly-permuted proteins by  
 PT scanning permutagenesis for generating libraries of permutins with  
 PT improved therapeutic properties -  
 XX  
 PS Claim 11; Page 40; 100pp; English.  
 XX

CC The preparation of biologically-activated circularly-permuted proteins  
 CC (permutins) comprises the use of a method comprising making a series of  
 CC circularly permuted genes. The circularly permuted genes are inserted  
 CC into a display vector, where they are expressed so that the proteins  
 CC they encode are presented on the surface of the display vector. A library  
 CC of display vectors presenting the expressed circularly permuted proteins  
 CC is generated. A target protein that can bind a biologically active  
 CC circularly permuted protein can be used to affinity select the  
 CC presenting display vectors. The selected display vectors can be isolated  
 CC and analysed to identify the presented circularly-permuted protein. The  
 CC permutins conform to the structure of a parent protein consisting of a  
 CC segment derived from the carboxy portion of the parent protein, a  
 CC linker or chemical bond linking the amino and carboxy terminal derived  
 CC portions. Nucleotide sequences AAA35576-A35943 encode linkers used to  
 CC create the permutins of the invention. The method is used to generate  
 CC libraries of permutins with improved therapeutic properties compared to  
 CC their parent molecules. Permutins with little or no activity may be used  
 CC as antigens for producing antibodies which are used in immunology or  
 CC immunotherapy as probes or intermediates used to construct other useful  
 CC permutins. Permutins have improved biological and therapeutic  
 CC properties compared to their two individual components due to alterations  
 CC in bio-distribution or half-life.  
 CC  
 SQ Sequence 36 BP; 3 A; 15 C; 10 G; 8 T; 0 other;  
 Query Match 58.5%; Score 15.2; DB 21; Length 36;  
 Best Local Similarity 85.0%; Pred. No. 1.5e+03;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 6 CATGCTTTGGTCCACGCTA 25  
 1 TGGTCATGCTTTGGTCCACGCTA 25  
 DB 9 CATGCTTTGGGCGCCCTGCCA 28  
 RESULT 10  
 AAL31378/c  
 ID AAL31378 standard; DNA; 50 BP.  
 XX  
 AC AAL31378;  
 XX  
 DT 24-JAN-2002 (first entry)  
 XX  
 DE Human SNP oligonucleotide #4586.  
 XX  
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 OS WO200147944-A2.  
 PN  
 XX 05-JUL-2001.  
 PD  
 XX 28-DEC-2000; 2000WO-US3498.  
 PF  
 XX 28-DEC-1999; 99US-0173419.  
 PR  
 XX 27-DEC-2000; 2000US-0173419.  
 PR  
 XX (CURA-) CURAGEN CORP.  
 PA  
 PI Shinkets RA, Leach M;  
 XX  
 DR WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amyases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 XX  
 PT



CC invention. The mahogany genes are used: (i) to produce recombinant  
CC mahogany (mg) proteins (II); (ii) as a source of antisense, ribozyme or  
CC triplex-forming therapeutics; (iii) as a source of diagnostic probes and  
CC primers for detecting expression of mg genes or mutations; regulatory  
CC defects in this gene, or for isolation of related sequences; and  
CC (iv) in (cell-based) gene therapy. (ii) are used to raise specific  
CC antibodies (Ab); to identify other (extra)cellular products involved in  
CC weight regulation, and to screen for agents that disrupt interaction  
CC between (II) and other macromolecules. The Ab are used to detect abnormal  
CC levels (or function) of (II) (for diagnosis, prognosis or monitoring of  
CC treatment); to evaluate (II)-expressing cells intended for cell therapy,  
CC and as therapeutic mg inhibitors. Cells that express the mg gene (or  
CC contain the mg polypeptide) are used to identify agents (A) that modulate  
CC mg activity. (A) are potentially useful for the treatment of body weight  
CC disorders, particularly obesity, cachexia or anorexia, or other  
CC conditions associated with the mg gene such as hyperpigmentation,  
CC hyperphagia and disorders that result in increased metabolic rate.  
XX  
SQ Sequence 28 BP; 13 A; 5 C; 6 G; 4 T; 0 other;

Query Match 57.7%; Score 15; DB 21; Length 28;  
Best Local Similarity 78.3%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGTCATGCTTTGGTCCACG 23  
||||| ||||| ||||| |||||  
DB 27 TGGTCATGCTTTTATCCACG 5

RESULT 13  
AAK36190/C  
ID AAK36190 standard; DNA; 44 BP.

AC AAK36190;  
XX  
DT 16-JUL-1999 (first entry)  
XX

DE Intronic location where the LTR trapping construct integrates.

XX  
XX  
XX Infectious virus; recombinant viral genome; chimeric integrase;  
KW mutagenesis; gene trapping; retroviral integration;  
KM provirus formation; ss.

XX Unidentified.

XX MO9907389-A1.

XX 18-FEB-1999.

XX 06-AUG-1998; 98WO-US16373.

XX 08-AUG-1997; 97US-0907598.

XX (LEXI-) LEXICON GENETICS INC.

XX Burgess R, Friedrich GA, Sands AT, Zambrowicz B;

XX WPI; 1999-287449/24.

PT New infectious viruses - comprising a recombinant viral genome and  
XX a chimeric integrase, used particularly for targeted gene discovery  
XX  
XX Disclosure: Fig 10B; 95pp; English.

XX The specification describes an infectious virus which comprises a  
CC recombinant viral genome and a chimeric integrase. The chimeric  
CC integrase can provide an infectious recombinant virus that is capable  
CC of infecting higher eukaryotic cells and incorporates a chimeric  
CC integrase activity that has been engineered to target and guide  
CC viral integration to specific regions of the genome of living cells.  
CC The viruses can be used in methods for the rapid identification and  
CC mutagenesis, via gene trapping, of genes encoding, regulated by, or  
CC adjacent to, target sequences for DNA binding proteins. They allow

CC for retroviral integration and provirus formation to occur at any  
CC location within the genome. By deleting the naturally occurring  
CC nonspecific DNA binding domain of the integrase, the amount of  
CC random integration of viral DNA into the host genome is reduced. This  
CC allows for a more efficient and high throughput analysis of target  
CC sites. The present sequence represents the sequence of the intronic  
CC location where the LTR trapping construct integrates.  
XX

SQ Sequence 44 BP; 9 A; 14 C; 12 G; 9 T; 0 other;

Query Match 57.7%; Score 15; DB 20; Length 44;  
Best Local Similarity 78.3%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGTCATGCTTTGGTCCACG 23  
||||| ||||| ||||| |||||  
DB 26 TAGCCATGCTTTAGTCCACG 4

RESULT 14  
AAL29694  
ID AAL29694 standard; DNA; 50 BP.

AC AAL29694;  
XX  
DT 24-JAN-2002 (first entry)  
XX

DE Human SNP oligonucleotide #2902.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
XX oncogenes and histones, useful for diagnosing and treating, e.g.  
XX cancer, autoimmune diseases and infections -  
XX  
XX Claim 1; Page 2217; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic  
CC variants of proteins related to amylases, amyloid proteins, angiotensin,  
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,  
CC histones, kinases, colony stimulating factors, complement related  
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,  
CC G-protein coupled receptors and thioesterases. The present sequence is  
CC one such oligonucleotide. The oligonucleotides and the peptides encoded  
CC by them may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate expression of the proteins listed  
CC above. Disorders that may be prevented, diagnosed and/or treated include  
CC multifactorial diseases with a genetic component, such as autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,

CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer  
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,  
 CC leukaemia), diseases of the nervous system and an infection of pathogenic  
 CC organisms.  
 CC

SQL Sequence 50 BP; 14 A; 11 C; 12 G; 13 T; 0 other;

Query Match 57.7%; Score 15; DB 22; Length 50;  
 Best Local Similarity 78.3%; Pred. No. 1.9e+03;  
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TGGTCATGTCCTTGGTCCAGC 23  
 DB 19 TGGTCATGTCCTGTAATCCAGC 41

## RESULT 15

ABN87593/c  
 ID ABN87593 standard; DNA; 41 BP.

AC ABN87593;

DT 07-AUG-2002 (first entry)

DE Oligodendrocyte-myelin glucoprotein 9.68 probe 2 SEQ ID NO:9.

KW Human; oligodendrocyte-myelin glucoprotein 9.68; probe; ss;  
 KW nervous system dysfunction related disease.

OS Homo sapiens.

PN CN1333225-A.

PD 30-JAN-2002.

PF 07-JUL-2000; 2000CN-0117081.

PR 07-JUL-2000; 2000CN-0117081.

PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.

PI Mao Y, Xie Y;

DR WPI; 2002-292915/34.

PT Novel polypeptide--oligodendrocyte-myelin glucoprotein 9.68 and  
 PT polynucleotide for encoding the polypeptide -

PS Example 6; Page 22 (Disclosure); 34pp; Chinese.

CC The present invention describes human oligodendrocyte-myelin glucoprotein  
 CC 9.68 (I). Also described is a method for producing (I) using DNA  
 CC recombination technology. (I) can be used in the treatment of several  
 CC diseases, such as nervous system dysfunction related diseases. The  
 CC present sequence represents a probe for (I), which is used in an  
 CC example from the present invention.  
 CC

SQL Sequence 41 BP; 5 A; 8 C; 16 G; 12 T; 0 other;

Query Match 56.9%; Score 14.8; DB 24; Length 41;  
 Best Local Similarity 73.1%; Pred. No. 2.3e+03;  
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TGGTCATGTCCTTGGTCCAGCTAC 26  
 DB 29 TGGACCAAGTCCAGGCCCACTTAC 4

Search completed: June 21, 2003, 22:26:21  
 Job time : 145.594 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 ; Search time 30.875 Seconds  
(without alignments)  
258.254 Million cell updates/sec

Title: US-09-964-666-10

Perfect score: 26  
Sequence: 1 TGGTGCAATGCTTTGGTCCAGCTAC 26

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCUTS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	17.6	67.7	47	US-09-641-638-660	Sequence 660, App
2	15.2	58.5	20	US-08-117-952-594	Sequence 594, App
3	15	57.7	28	US-09-245-041-105	Sequence 105, App
4	15	57.7	44	US-08-907-598-10	Sequence 10, Appl
5	14.8	56.9	20	US-09-851-896-84	Sequence 84, Appl
6	14.8	56.9	36	US-07-971-819A-32	Sequence 32, Appl
7	14.8	56.9	36	US-07-977-434-28	Sequence 32, Appl
8	14.8	56.9	36	US-08-475-231-32	Sequence 32, Appl
9	14.8	56.9	36	US-08-458-819-28	Sequence 28, Appl
10	14.8	56.9	36	PCR-US91-07035-28	Sequence 28, Appl
11	14.4	55.4	20	US-08-223-177A-270	Sequence 270, App
12	14.4	55.4	41	US-08-239-256-18	Sequence 18, App
13	14.4	55.4	41	5177193-20	Patent No. 5177193
14	14.2	54.6	42	US-09-286-959B-12	Sequence 12, Appl
15	14.2	54.6	42	US-08-283-857-9	Sequence 9, Appl
16	13.6	52.3	33	US-09-461-697-134	Sequence 134, App
17	13.6	52.3	38	US-08-963-946-10	Sequence 10, Appl
18	13.6	52.3	39	US-08-963-946-8	Sequence 8, Appl
19	13.6	52.3	39	US-08-964-020-12	Sequence 12, Appl
20	13.4	51.5	17	US-09-286-529-11	Sequence 11, Appl
21	13.4	51.5	21	US-09-306-998-8	Sequence 8, Appl
22	13.4	51.5	30	US-08-503-062-24	Sequence 24, Appl
23	13.4	51.5	30	PCR-US96-11495-24	Sequence 24, Appl
24	13.4	51.5	35	US-08-463-224-43	Sequence 43, Appl
25	13.4	51.5	35	US-08-463-377-43	Sequence 43, Appl
26	13.4	51.5	39	US-08-463-224-44	Sequence 44, Appl
27	13.4	51.5	39	US-08-463-377-44	Sequence 44, Appl

28	13.4	51.5	40	US-07-927-391-21	Sequence 21, Appl
29	13.2	50.8	32	US-07-987-264-18	Sequence 18, Appl
30	13.2	50.8	40	US-07-987-264-24	Sequence 24, Appl
31	13.2	50.8	43	US-09-489-979-2	Sequence 2, Appl
32	13.2	50.8	49	US-09-302-620B-76	Sequence 76, Appl
33	13	50.0	28	US-09-609-816-21	Sequence 21, Appl
34	13	50.0	29	US-08-295-676A-15	Sequence 15, Appl
35	13	50.0	29	US-08-948-591-15	Sequence 15, Appl
36	13	50.0	32	US-08-362-525-5	Sequence 5, Appl
37	13	50.0	47	US-09-641-638-1157	Sequence 1157, Ap
38	13	50.0	50	5464943-3	Patent No. 5464943
39	12.8	49.2	18	US-09-071-433-57	Sequence 57, Appl
40	12.8	49.2	25	US-08-348-891A-16	Sequence 16, Appl
41	12.8	49.2	25	US-08-905-817-16	Sequence 16, Appl
42	12.8	49.2	29	US-08-471-058-4	Sequence 4, Appl
43	12.8	49.2	29	US-08-471-057-4	Sequence 4, Appl
44	12.8	49.2	34	US-08-178-476A-17	Sequence 17, Appl
45	12.8	49.2	34	US-08-257-073-136	Sequence 136, App

## ALIGNMENTS

```

RESULT 1
US-09-641-638-660
; Sequence 660, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GENSET, 051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; PRIOR APPLICATION NUMBER: 2000-08-16
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 660
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-500-258 : polymorphic base G or T
; NAME/KEY: misc-feature
; LOCATION: 1
; OTHER INFORMATION: n=a, g, c or t
US-09-641-638-660

Query Match          67.7% Score 17.6; DB 4; Length 47;
Best Local Similarity 76.9% Pred No. 13;
Matches 20; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 TGGTGCAATGCTTTGGTCCAGCTAC 26
        |||||  ||| : |||||
Db       13 TGGTGCAATGCTTTGGTCCAGCTAC 38

RESULT 2
US-08-117-952-594/c
; Sequence 594, Application US/08117952
; Patent No. 5851760

```

GENERAL INFORMATION:  
APPLICANT: Evans, Glen A.  
APPLICANT: Smith, Michael W.  
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE  
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES  
NUMBER OF SEQUENCES: 797  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
STREET: 444 South Flower Street, Suite 2000  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,952  
FILING DATE: 07-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/078,471  
FILING DATE: 15-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Reiter, Stephen E.  
REGISTRATION NUMBER: 31,192  
REFERENCE/DOCKET NUMBER: P41 9423  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-546-4737  
TELEFAX: 619-546-9392  
INFORMATION FOR SEQ ID NO: 594:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Oligonucleotide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-117-952-594

Query Match 58.5%; Score 15.2; DB 2; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGCTTGTGCTCCAGCTAC 26  
DB 20 ATCCCTGTGCTCCAGCTAC 1

RESULT 3  
US-09-245-041-105/C  
Sequence 105, Application US/09245041  
GENERAL INFORMATION:  
APPLICANT: Moore, K.  
APPLICANT: Nagle, D.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT  
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY  
FILE REFERENCE: 7853-136  
CURRENT APPLICATION NUMBER: US/09/245,041  
CURRENT FILING DATE: 1999-02-05  
EARLIER APPLICATION NUMBER: 60/093,630  
EARLIER FILING DATE: 1998-07-21  
EARLIER APPLICATION NUMBER: 60/104,978  
NUMBER OF SEQ ID NOS: 131  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 105  
LENGTH: 281  
TYPE: DNA

ORGANISM: Artificial sequence  
US-09-245-041-105

Query Match 57.7%; Score 15; DB 4; Length 28;  
Best Local Similarity 78.3%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGTGTCATGCTTGTGCTCCAGC 23  
DB 27 TGTGTCATGCTTGTATCCAGC 5

RESULT 4  
US-08-907-598-10/C  
Sequence 10, Application US/08907598  
Patent No. 6139833  
GENERAL INFORMATION:  
APPLICANT: Burgess, Rob  
APPLICANT: Friedrich, Glenn  
APPLICANT: Zambrowicz, Brian  
APPLICANT: Sands, Arthur  
TITLE OF INVENTION: TARGETED GENE DISCOVERY  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/907,598  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8535-015-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 493-4935  
TELEFAX: (650) 493-5556  
TELEX: 66141  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: NO  
US-08-907-598-10

Query Match 57.7%; Score 15; DB 3; Length 44;  
Best Local Similarity 78.3%; Pred. No. 2.1e+02;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGTGTCATGCTTGTGCTCCAGC 23  
DB 26 TAGCCATGCTTGTAGTCCAGC 4

RESULT 5  
US-09-851-896-84  
Sequence 84, Application US/09851896  
Patent No. 6410325  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Susan M. Freiler

APPLICANT: Andrew T. Watt  
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPENDENT)  
FILE REFERENCE: RUS-0220  
CURRENT APPLICATION NUMBER: US/09/851,896  
CURRENT FILING DATE: 2001-05-08  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 84  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-851-896-84

Query Match 56.9%; Score 14.8; DB 4; Length 20;  
Best Local Similarity 88.9%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 CATGCTTTGGTCCAGC 23  
1 CATTTCTTAGTCCAGC 18

Db 1 CATTTCTTAGTCCAGC 18

RESULT 6  
US-07-971-819A-32  
Sequence 32, Application US/07971819A  
Patent No. 5420029  
GENERAL INFORMATION:  
APPLICANT: Gelfand, David H.  
APPLICANT: Lawyer, Frances C.  
APPLICANT: Stoffel, Susanne  
TITLE OF INVENTION: Purified Thermostable Nucleic Acid  
TITLE OF INVENTION: Polymerase Enzyme from Thermotoga Maritima  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/971,819A  
FILING DATE: 19930203  
CLASSIFICATION: A35  
ATTORNEY/AGENT INFORMATION:  
NAME: Stacey R. Sias, Ph.D.  
REGISTRATION NUMBER: 32,630  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2863  
TELEFAX: (510) 814-2977  
TELEX:  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other Nucleic Acid  
US-07-971-819A-32

Query Match 56.9%; Score 14.8; DB 1; Length 36;  
Best Local Similarity 73.1%; Pred. No. 2.5e+02;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TGGTGATGCTCTTGTGTCACGCTAC 26

Db 2 TGAACCATGCTTTGTGTCACGCTAC 27

RESULT 7  
US-07-977-434-28  
Sequence 28, Application US/07977434  
Patent No. 546591  
GENERAL INFORMATION:  
APPLICANT: Gelfand, David H.  
APPLICANT: Adrison, Richard D.  
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7  
SOFTWARE: Wordperfect 2.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/977,434  
FILING DATE:  
CLASSIFICATION: A35  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,490  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,466  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 590,213  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 523,394  
FILING DATE: 15-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 143,441  
FILING DATE: 12-JAN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 063,509  
FILING DATE: 17-JUN-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,241  
FILING DATE: 22-AUG-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 746,121  
FILING DATE: 15-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US90/07641  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 585,471  
FILING DATE: 20-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 455,611  
FILING DATE: 22-DEC-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 609,157  
FILING DATE: 02-NOV-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 557,517  
FILING DATE: 24-JUL-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Luann Casert  
REGISTRATION NUMBER: 31,822  
REFERENCE/DOCKET NUMBER: Case No. 546591 8753  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 814-2972  
 INFORMATION FOR SEQ ID NO: 28:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA primer FL64  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-07-977-434-28

Query Match 56.9%; Score 14.8; DB 1; Length 36;  
 Best Local Similarity 73.1%; Pred. No. 2.5e+02;  
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGGTGCATGCTTTGGTCCACGTAC 26  
 11 1111111111 11 111  
 DB 2 TGAGCATGCTTTGTCCACGGTTAC 27

RESULT 8  
 US-08-475-231-32  
 Sequence 32, Application US/08475231  
 Patent No. 5624833

GENERAL INFORMATION:  
 APPLICANT: Gelfand, David H.  
 APPLICANT: Lawyer, Frances C.  
 APPLICANT: Stoffel, Susanne  
 TITLE OF INVENTION: Purified Thermostable Nucleic Acid  
 TITLE OF INVENTION: Polymerase Enzyme from Thermotoga Maritima  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hoffmann-La Roche Inc.  
 STREET: 340 Kingsland Street  
 CITY: Nutley  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07110-1199  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 7  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/475,231  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/971,819  
 FILING DATE: 03-FEB-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stacey R. Sias, Ph.D.  
 REGISTRATION NUMBER: 32,630  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (510) 814-2863  
 TELEFAX: (510) 814-2977  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 32:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Other Nucleic Acid  
 US-08-475-231-32

Query Match 56.9%; Score 14.8; DB 1; Length 36;  
 Best Local Similarity 73.1%; Pred. No. 2.5e+02;  
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGGTGCATGCTTTGGTCCACGTAC 26

DB 11 1111111111 11 111  
 2 TGAGCATGCTTTGTCCACGGTTAC 27

RESULT 9  
 US-08-458-819-28  
 Sequence 28, Application US/08458819  
 Patent No. 5795762  
 GENERAL INFORMATION:  
 APPLICANT: Gelfand, David H.  
 APPLICANT: Abramson, Richard D.  
 TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF  
 NUMBER OF SEQUENCES: 38  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Hoffmann-La Roche Inc.  
 STREET: 340 Kingsland Street  
 CITY: Nutley  
 STATE: New Jersey  
 ZIP: 07110-1199  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Macintosh  
 OPERATING SYSTEM: 7  
 SOFTWARE: WordPerfect 2.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/458,819  
 FILING DATE: 02-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/977,434  
 FILING DATE: 23-FEB-1993  
 APPLICATION NUMBER: US 590,490  
 FILING DATE: 28-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 590,466  
 FILING DATE: 28-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 590,213  
 FILING DATE: 28-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 523,394  
 FILING DATE: 15-MAY-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 143,441  
 FILING DATE: 12-JAN-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 063,509  
 FILING DATE: 17-JUN-1987  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 899,241  
 FILING DATE: 22-AUG-1986  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 746,121  
 FILING DATE: 15-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US90/07641  
 FILING DATE: 21-DEC-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 585,471  
 FILING DATE: 20-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 455,611  
 FILING DATE: 22-DEC-1989  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 609,157  
 FILING DATE: 02-NOV-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 557,517  
 FILING DATE: 24-JUL-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Luann Cseer  
 REGISTRATION NUMBER: 31,822





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? TELEFAX: (608) 831-2106
? TELEX:
? INFORMATION FOR SEQ ID NO: 270
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 20 base pairs
?
? TYPE: nucleic acid
?
? STRANDEDNESS: double
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: DNA (genomic)
?
? IMMEDIATE SOURCE:
?
? CLONE: mcd7bp2
?
US-08-222-177A-270

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Query Match	55.48;	Score 14.4;	DB 1;	Length 20
Best Local Similarity	93.88;	Pred. No. 3.6e+02;		
Matches 15; Conservative	0;	Mismatches 1;	Indels	

QY	8	TGCTTTGGTCCAGC	23
Db	4	TGCTATGGTCCAGC	19

RESULT 12  
US-08-239-256-18

Sequence 18, Application US/08239256  
Patent No. 5585345  
GENERAL INFORMATION:  
APPLICANT: BOIME, IRVING  
APPLICANT: MATZUK, MARTIN M.  
APPLICANT: KEENE, JEFFREY L.  
TITLE OF INVENTION: CTP EXTENDED FORM OF LHM  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave. N.W.  
CITY: Washington, D.C.

Query Match	55.48;	Score 14.4;	DB 1;	Length 41;
Best Local Similarity	75.08;	Pred. No. 4e+02;		
Matches 18; Conservative	0;	Mismatches 6;	Indels	

QY		3	GTGCATGCTCTTGGTGTCACAGCTAC	26
Db		7	GTGCGAGGCTTGGGCCACAGCTAC	30

## RESÜLT 13

5177193-20  
; Patent No. 5177193  
; APPLICANT: BOIME, IRVING; MATZUK, MARTIN M.  
; TITLE OF INVENTION: MODIFIED FORMS OF REPRODUCTIVE HORMONES  
; NUMBER OF SEQUENCES: 26  
; CITESEQUENCE ADDITION DATA:

Query Match	55.4%	Score 14.4	DB 6	Length 41
Best Local Similarity	75.0%	Pred. No. 4e+02		
Matches 18	Conservative 0	Mismatches 6	Indels 0	Gaps 0

QY	3	GTGCATGTCCTTGGTCCAGCTAC	26
Db	7	GTGCGAGGCGCTGGGCCAGCTAC	30

RESULT 14  
US-09-286-959B-12  
; Sequence 12, Application US/09286959B

```

1 Patent No. 6300131
2
3 GENERAL INFORMATION:
4
5 APPLICANT: Johns Hopkins University
6
7 APPLICANT: Greider, Carol W.
8
9 APPLICANT: Ie, Siyuan
10
11 TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
12
13 FILE REFERENCE: 07265/157001
14
15 CURRENT APPLICATION NUMBER: US/09/286,959B
16
17 CURRENT FILING DATE: 1999-04-06
18
19 PRIOR APPLICATION NUMBER: 60/080,783
20
21 PRIOR FILING DATE: 1998-04-06
22
23 NUMBER OF SEQ ID NOS: 24
24
25 SOFTWARE: FastSeq for Windows Version 4.0
26
27 SEQ ID NO 12
28
29 LENGTH: 20
30
31 TYPE: DNA
32
33 ORGANISM: Artificial Sequence
34
35 FEATURE:
36
37 OTHER INFORMATION: Primer
38
39 US-09-286-959B-12

```

Query Match	54.6%	Score 14.2	DB 4:	Length 20:
Best Local Similarity	84.2%	Pred. No. 4.4e+02:		
Matches 16, Conservative	0	Mismatches 3:	Indels 0:	Gaps 0:

QY	8	TGTCTTTGGTCCAGCTAC	26
Db	2	TGCCTGTAGTCCAGCTAC	20

RESULT 15  
US-08-283-857-9/c

Sequence 9, Application US/0823857  
Patent No. 5792742  
GENERAL INFORMATION:  
APPLICANT: GOLD, Leslie I.  
APPLICANT: ROSTAGNO, Agueda A.  
APPLICANT: BARON, Martin  
APPLICANT: CAMPBELL, Iain D.  
APPLICANT: WILLIAMS, Michael, J.  
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNASE  
TITLE OF INVENTION: CODING THEREFOR AND USERS THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NETMARK  
STREET: 419 Seventh Street, N.W., Suite 300

```

: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/283,857
: FILING DATE: 01-AUG-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/714,134
: FILING DATE: 14-JUN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: GOLD=1A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 42 nucleotides
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-08-283-857-9

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Query Match          54.6%; Score 14.2; DB 1; Length 42;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      6 CATGCTTTGGTCCAGCT 24
       111 111111111 111
Db      26 CATCTCTTTTGTCCAAGCT 8

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 Job time : 32.875 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 22:26:37 ; Search time 76.7812 Seconds  
(without alignments)  
496.907 Million cell updates/sec

Title: US-09-964-666-10

Perfect score: 26  
Sequence: 1 TGGTCAGATGCTTTGGTCCAGACTAC 26

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA.\*  
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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
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14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	26	100.0	26	10	US-09-964-666-10
3	26	100.0	26	10	US-09-964-412-10
4	21	80.8	39	9	US-10-198-069-46
5	15	57.7	28	10	US-09-893-238-105
6	14.8	56.9	25	9	US-10-098-263B-127897
7	14.6	56.2	23	9	US-09-860-738C-35
8	14.6	56.2	23	9	US-09-860-738C-38
9	14.6	56.2	23	9	US-09-860-738C-48
10	14.6	56.2	23	9	US-09-860-738C-50
11	14.6	56.2	23	9	US-09-860-738C-53
12	14.6	56.2	23	9	US-09-860-738C-55
13	14.6	56.2	23	9	US-09-860-738C-74
14	14.6	56.2	23	9	US-10-198-069-45
15	14.6	56.2	41	9	US-09-860-738C-36
16	14.6	56.2	41	9	US-09-860-738C-54
17	14.2	54.6	25	9	US-10-098-263B-50917
18	14	53.8	25	9	US-10-098-263B-104291
19	14	53.8	31	10	US-09-801-274-450

20	14	53.8	31	10	US-09-801-274-1391	Sequence 1391, Ap
21	14	53.8	37	9	US-10-001-876-109	Sequence 109, App
22	13.8	53.1	42	9	US-09-733-692A-30	Sequence 30, Appl
23	13.6	52.3	25	9	US-10-098-263B-23537	Sequence 23537, A
24	13.6	52.3	35	9	US-10-098-263B-130235	Sequence 130235,
25	13.6	52.3	31	10	US-09-801-274-1127	Sequence 1727, Ap
26	13.6	52.3	33	10	US-09-922-261-134	Sequence 134, App
27	13.4	51.5	17	10	US-09-877-156-11	Sequence 11, Appl
28	13.4	51.5	21	9	US-09-951-402-8	Sequence 8, Appl
29	13.4	51.5	21	10	US-09-951-401-8	Sequence 8, Appl
30	13.4	51.5	21	10	US-09-922-101-8	Sequence 8, Appl
31	13.4	51.5	25	9	US-10-098-263B-1457	Sequence 1457, Ap
32	13.4	51.5	25	9	US-10-098-263B-105579	Sequence 105579,
33	13.4	51.5	25	9	US-10-098-263B-121069	Sequence 121069
34	13.4	51.5	31	9	US-09-912-263-435	Sequence 435, App
35	13.4	51.5	32	10	US-09-795-006A-4	Sequence 4, Appl
36	13.4	51.5	37	9	US-09-780-164-1792	Sequence 1792, Ap
37	13.4	51.5	42	10	US-09-795-006A-13	Sequence 13, Appl
38	13.2	50.8	22	9	US-10-198-069-39	Sequence 39, Appl
39	13.2	50.8	25	9	US-10-098-263B-36336	Sequence 36336, A
40	13.2	50.8	25	9	US-10-098-263B-59077	Sequence 59077, A
41	13.2	50.8	25	9	US-10-098-263B-76416	Sequence 76416, A
42	13.2	50.8	25	9	US-10-098-263B-11162	Sequence 11162,
43	13.2	50.8	25	9	US-10-098-263B-116373	Sequence 116373,
44	13.2	50.8	25	9	US-10-098-263B-127898	Sequence 127898,
45	13.2	50.8	28	9	US-10-198-069-38	Sequence 38, Appl

## ALIGNMENTS

RESULT 1  
US-09-964-667-10  
Sequence 10, Application US/09964667  
Publication No. US20030033621A1  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
Mands, Jack R.  
TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/964,667  
FILING DATE: 28-Sep-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0609,4370000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-964-667-10

Query Match 100.0%; Score 26; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTGCATGCTTTGGTCCACGCTAC 26  
|||||

DB 1 TGGTGCATGCTTTGGTCCACGCTAC 26

RESULT 2

US-09-964-666-10

Sequence 10, Application US/09964666

Patent No. US20020104108A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-964-666-10

Query Match 100.0%; Score 26; DB 10; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTGCATGCTTTGGTCCACGCTAC 26  
|||||

DB 1 TGGTGCATGCTTTGGTCCACGCTAC 26

RESULT 3

US-09-964-412-10

Sequence 10, Application US/09964412

Patent No. US20020129391A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-964-412-10

Query Match 100.0%; Score 26; DB 10; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.0055;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 TGGTGCATGCTTTGGTCCACGCTAC 26  
|||||

DB 1 TGGTGCATGCTTTGGTCCACGCTAC 26

RESULT 4

US-10-198-069-46/c

Sequence 46, Application US/10198069

Publication No. US20030096756A1

GENERAL INFORMATION:

APPLICANT: AVERBACK, PAUL

TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER

CONDITIONS, REQUIRING THE REMOVAL OR DESTRUCTION OF

FILE REFERENCE: 59003.000009

CURRENT APPLICATION NUMBER: US/10/198,069

CURRENT FILING DATE: 2002-07-19

PRIOR APPLICATION NUMBER: 60/306,161

PRIOR FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 60/306,150

PRIOR FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 60/331,477

PRIOR FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 46

LENGTH: 39

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-198-069-46

Query Match 80.8%; Score 21; DB 9; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CATGCTTGTGCTCCAGCTAC 26  
DB 39 CATGCTTGTGCTCCAGCTAC 19

## RESULT 5

US-09-893-238-105/c  
; Sequence 105, Application US/09893238  
; Patent No. US20020150973A1  
; GENERAL INFORMATION:  
; APPLICANT: Moore, K.  
; APPLICANT: Moore, K.  
; APPLICANT: Nagle, D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND  
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
; FILE REFERENCE: 7853-237  
; CURRENT APPLICATION NUMBER: US/09/893,238  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: 09/245,041  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 60/093,630  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: 60/104,978  
; PRIOR FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 105  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-893-238-105

Query Match 57.7%; Score 15; DB 10; Length 28;  
Best Local Similarity 78.3%; Pred. No. 8.7e+02;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGTCATGCTCTTGGTCCAGC 23  
DB 27 TGGTCATGCTCTTGGTCCAGC 5

## RESULT 6

US-10-098-263B-127897  
; Sequence 127897, Application US/10098263B  
; Publication No. US20030104410A1  
; GENERAL INFORMATION:  
; APPLICANT: Miltman, Michael  
; TITLE OF INVENTION: Human Microarray  
; FILE REFERENCE: 3118.1  
; CURRENT APPLICATION NUMBER: US/10/098,263B  
; CURRENT FILING DATE: 2003-01-08  
; PRIOR APPLICATION NUMBER: 60/276,759  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 131066  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 127897  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-098-263B-127897

Query Match 56.9%; Score 14.8; DB 9; Length 25;  
Best Local Similarity 88.9%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTGCATGCTTGTGCTCC 20  
DB 4 GTGCAGTCTTGGTCC 21

## RESULT 7

US-09-860-738C-35  
; Sequence 35, Application US/09860738C  
; Publication No. US20030040620A1  
; GENERAL INFORMATION:  
; APPLICANT: Langmore, John  
; APPLICANT: Langmore, John  
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplificati  
; FILE REFERENCE: UMIC:047US0/10103482  
; CURRENT APPLICATION NUMBER: US/09/860,738C  
; CURRENT FILING DATE: 2001-05-18  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-860-738C-35

Query Match 56.2%; Score 14.6; DB 9; Length 23;  
Best Local Similarity 81.0%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTGCATGCTTGTGCTCCAG 22  
DB 2 GTGCATGCTTGTGCTCCAG 22

## RESULT 8

US-09-860-738C-38  
; Sequence 38, Application US/09860738C  
; Publication No. US20030040620A1  
; GENERAL INFORMATION:  
; APPLICANT: Langmore, John  
; APPLICANT: Langmore, John  
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplificati  
; FILE REFERENCE: UMIC:047US0/10103482  
; CURRENT APPLICATION NUMBER: US/09/860,738C  
; CURRENT FILING DATE: 2001-05-18  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-860-738C-38

Query Match 56.2%; Score 14.6; DB 9; Length 23;  
Best Local Similarity 81.0%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTGCATGCTTGTGCTCCAG 22  
DB 2 GTGCATGCTTGTGCTCCAG 22

## RESULT 9

US-09-860-738C-48  
; Sequence 48, Application US/09860738C  
; Publication No. US20030040620A1  
; GENERAL INFORMATION:  
; APPLICANT: Langmore, John  
; APPLICANT: Langmore, John  
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplificati  
; FILE REFERENCE: UMIC:047US0/10103482  
; CURRENT APPLICATION NUMBER: US/09/860,738C  
; CURRENT FILING DATE: 2001-05-18

NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 48  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-860-738C-48

Query Match 56.2% Score 14.6; DB 9; Length 23;  
Best Local Similarity 81.0% Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATGCTTGTGTCGAG 22  
||||||| | | | | |  
Db 2 GGTCATGCTGTATCGTCCGAG 22

RESULT 10  
US-09-860-738C-50  
Sequence 50, Application US/09860738C  
Publication No. US20030040620A1  
GENERAL INFORMATION:  
APPLICANT: Langmore, John  
TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification  
FILE REFERENCE: UMIC:047US0/10103482  
CURRENT APPLICATION NUMBER: US/09/860,738C  
CURRENT FILING DATE: 2001-05-18  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 50  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-860-738C-50

Query Match 56.2% Score 14.6; DB 9; Length 23;  
Best Local Similarity 81.0% Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATGCTTGTGTCGAG 22  
||||||| | | | | |  
Db 2 GGTCATGCTGTATCGTCCGAG 22

RESULT 11  
US-09-860-738C-53  
Sequence 53, Application US/09860738C  
Publication No. US20030040620A1  
GENERAL INFORMATION:  
APPLICANT: Langmore, John  
TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification  
FILE REFERENCE: UMIC:047US0/10103482  
CURRENT APPLICATION NUMBER: US/09/860,738C  
CURRENT FILING DATE: 2001-05-18  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 53  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-860-738C-53

Query Match 56.2% Score 14.6; DB 9; Length 23;  
Best Local Similarity 81.0% Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATGCTTGTGTCGAG 22  
||||||| | | | | |  
Db 2 GGTCATGCTGTATCGTCCGAG 22

RESULT 12  
US-09-860-738C-55  
Sequence 55, Application US/09860738C  
Publication No. US20030040620A1  
GENERAL INFORMATION:  
APPLICANT: Langmore, John  
TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification  
FILE REFERENCE: UMIC:047US0/10103482  
CURRENT APPLICATION NUMBER: US/09/860,738C  
CURRENT FILING DATE: 2001-05-18  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 55  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-860-738C-55

Query Match 56.2% Score 14.6; DB 9; Length 23;  
Best Local Similarity 81.0% Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATGCTTGTGTCGAG 22  
||||||| | | | | |  
Db 2 GGTCATGCTGTATCGTCCGAG 22

RESULT 13  
US-09-860-738C-74  
Sequence 74, Application US/09860738C  
Publication No. US20030040620A1  
GENERAL INFORMATION:  
APPLICANT: Langmore, John  
TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification  
FILE REFERENCE: UMIC:047US0/10103482  
CURRENT APPLICATION NUMBER: US/09/860,738C  
CURRENT FILING DATE: 2001-05-18  
NUMBER OF SEQ ID NOS: 121  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 74  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-860-738C-74

Query Match 56.2% Score 14.6; DB 9; Length 23;  
Best Local Similarity 81.0% Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTCATGCTTGTGTCGAG 22  
||||||| | | | | |  
Db 2 GGTCATGCTGTATCGTCCGAG 22

RESULT 14  
US-10-198-069-45/C  
Sequence 45, Application US/10198069  
Publication No. US20030096756A1  
GENERAL INFORMATION:  
APPLICANT: AVERBACK, PAUL  
TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER



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; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO: 45
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-198-069-45

```

```

Query Match      56.2%   Score 14.6;   DB 9;   Length 39;
Best Local Similarity 81.0%;   Pred. No. 1.4e+03;
Matches 17;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

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OY      6 CATGCTTGTGTCCTCCAGCTAC 26
      ||| || | |||||
Db      39 CATGCTGTATCTCCAGCTAC 19

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RESULT 15
US-09-860-738C-36/c
; Sequence 36, Application US/09860738C
; Publication No. US20030040620A1
; GENERAL INFORMATION:
; APPLICANT: Langmore, John
; APPLICANT: Makarov, Vladimir
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
; FILE REFERENCE: UMC:047US0/10103482
; CURRENT APPLICATION NUMBER: US/09/860,738C
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentln version 3.1
; SEQ ID NO: 36
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Primer
US-09-860-738C-36

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```

Query Match      56.2%   Score 14.6;   DB 9;   Length 41;
Best Local Similarity 81.0%;   Pred. No. 1.4e+03;
Matches 17;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

```

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OY      2 GGTCATGCTTGTGTCAG 22
      ||||| | | |||
Db      40 GGTCATGTATCTCCAG 20

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 Job time : 78,7812 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:28:37 ; Search time 1123.08 Seconds  
(without alignments)  
374.936 Million cell updates/sec

Title: US-09-964-666-10

Perfect score: 26  
Sequence: 1 TCGTCATGCTTTGGTCCACACTAC 26

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
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6: em\_estopl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	18	69.2	40	14	N95034 zb32b05.s1
C 3	18	69.2	45	14	T92229 ye17f11.r1
4	17	65.4	48	14	N79917 yz86a06.r1
5	16.8	64.6	33	14	H85333 ys90e04.r1
C 6	16.6	63.8	34	17	AZ393855 IM0157D07

7	16.6	63.8	48	17	AZ496155
C 8	16.2	62.3	32	14	T92842
C 9	16.2	62.3	32	14	T92862
C 10	15.6	60.0	24	17	AZ831249
C 11	15.2	58.5	28	14	T94044
C 12	15.2	58.5	28	14	T94189
C 13	15.2	58.5	33	14	N67043
14	15	57.7	38	17	AZ438336
C 15	15	57.7	41	17	AZ489704
C 16	15	57.7	42	9	AA868654
C 17	15	57.7	43	14	H09843
C 18	15	57.7	43	14	R61212
C 19	15	57.7	46	17	AZ471093
C 20	14.8	56.9	34	14	N63645
C 21	14.8	56.9	50	9	AU102380
C 22	14.4	55.4	31	17	AZ393553
C 23	14.2	54.6	50	9	AU102523
C 24	14.2	54.6	50	17	AZ809862
C 25	14	53.8	24	17	AZ822910
C 26	14	53.8	50	14	H60434
C 27	13.8	53.1	25	17	AZ635949
C 28	13.8	53.1	47	17	AL754182
C 29	13.8	53.1	49	9	AA458130
C 30	13.6	52.3	28	14	H70161
C 31	13.6	52.3	42	14	R84748
C 32	13.6	52.3	43	14	H69549
C 33	13.6	52.3	47	14	R55441
C 34	13.4	51.5	28	17	AZ361627
C 35	13.4	51.5	31	17	AZ659725
C 36	13.4	51.5	32	14	H46868
C 37	13.4	51.5	38	13	B1112512
C 38	13.4	51.5	50	9	AU102375
C 39	13.4	51.5	50	9	AU102386
C 40	13.4	51.5	50	14	N26705
C 41	13.2	50.8	33	13	BM392790
C 42	13.2	50.8	33	13	BM394082
C 43	13.2	50.8	36	14	R44635
C 44	13.2	50.8	50	9	AU102384
45	13	50.0	24	17	TA57D02P

## ALIGNMENTS

RESULT 1  
LOCUS H47110/c 42 bp mRNA linear EST 16-AUG-1995  
DEFINITION yp77603.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:193468 3' similar to gb:213009\_rnal EPITHELIAL-CADHERIN  
PRECURSOR (HUMAN); mRNA sequence.

ACCESSION H47110  
VERSION H47110.1 GI:923162

KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 42)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
Insert Size: 704  
High quality sequence starts: 1  
High quality sequence starts: 1

## TITLE

JOURNAL  
COMMENT







with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 21 c 8 g 7 t

Query Match 63.8%; Score 16.6; DB 17; Length 48;  
Best Local Similarity 82.6%; Pred. No. 4.6e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TGGTCATGCTTGTGTCACAGC 23  
||||| ||||| |||||  
Db 23 TGTGTCAGCGCTTATATCCAGC 1

RESULT 8  
T92842/c  
LOCUS  
DEFINITION T92842 32 bp mRNA linear EST 22-MAR-1995  
ye27a08.r1 Stratagene lung (#937210) Homo sapiens cDNA clone  
IMAGE:118934.5' similar to gb:213009\_rn1 EPITHELIAL-CADHERIN  
PRECUSOR (HUMAN);, mRNA sequence.

ACCESSION T92842 GI:724755  
VERSION T92842.1  
KEYWORDS EST;  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chapell,B.,  
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,  
'M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,  
'B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,  
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,E.,  
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
97044478

TITLE JOURNAL  
MEDLINE  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
Insert Size: 451  
High quality sequence starts: 1 High quality sequence stops: 1  
Source: IMAGE Consortium, LNL This clone is available royalty-free  
through LNL; contact the IMAGE Consortium (info@image.lnl.gov)  
for further information. Trace considered overall poor quality  
Insert length: 451 Std Error: 0.00  
Seq primer: M13RP1

FEATURES  
source High quality sequence stop: 1.  
Location/Qualifiers  
1..32  
/organism="Homo sapiens"  
/db\_xref="GDB:487223"  
/db\_xref="taxon:9606"  
/clone="IMAGE:118934"  
/clone\_lib="Stratagene lung (#937210)"  
/sex="male"  
/dev\_stage="72 years"  
/lab\_host="SOLR cells (kanamycin resistant)"  
/note="Organ: Lung; Vector: pBluescript SK-; Site:1: EcoRI  
; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo  
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR  
Vector; -5' adaptor sequence: 5' GAATTCGCGCAG 3' -3'  
adaptor sequence: 5' CTCGAGCTTTT 3' "

BASE COUNT 9 a 10 c 8 g 5 t

Query Match 62.3%; Score 16.2; DB 14; Length 32;

Best Local Similarity 85.7%; Pred. No. 6.2e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CATGCTTTGGTCCAGCTAC 26  
||||| ||||| |||||  
Db 32 CATGCTATGCTCTAGCTAC 12

RESULT 9  
T92862/c  
LOCUS  
DEFINITION T92862 32 bp mRNA linear EST 22-MAR-1995  
ye27e08.r1 Stratagene lung (#937210) Homo sapiens cDNA clone  
IMAGE:118982.5' similar to gb:213009\_rn1 EPITHELIAL-CADHERIN  
PRECUSOR (HUMAN);, mRNA sequence.

ACCESSION T92862 GI:724775  
VERSION T92862.1  
KEYWORDS EST;  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chapell,B.,  
Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,  
'M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,  
'B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,  
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,E.,  
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
97044478

TITLE JOURNAL  
MEDLINE  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
Insert Size: 565  
High quality sequence starts: 1 High quality sequence stops: 1  
Source: IMAGE Consortium, LNL This clone is available royalty-free  
through LNL; contact the IMAGE Consortium (info@image.lnl.gov)  
for further information. Trace considered overall poor quality  
Insert length: 565 Std Error: 0.00  
Seq primer: M13RP1

FEATURES  
source High quality sequence stop: 1.  
Location/Qualifiers  
1..32  
/organism="Homo sapiens"  
/db\_xref="GDB:487271"  
/db\_xref="taxon:9606"  
/clone="IMAGE:118982"  
/clone\_lib="Stratagene lung (#937210)"  
/sex="male"  
/dev\_stage="72 years"  
/lab\_host="SOLR cells (kanamycin resistant)"  
/note="Organ: Lung; Vector: pBluescript SK-; Site:1: EcoRI  
; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo  
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR  
Vector; -5' adaptor sequence: 5' GAATTCGCGCAG 3' -3'  
adaptor sequence: 5' CTCGAGCTTTT 3' "

BASE COUNT 9 a 10 c 8 g 5 t

Query Match 62.3%; Score 16.2; DB 14; Length 32;  
Best Local Similarity 85.7%; Pred. No. 6.2e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CATGCTTTGGTCCAGCTAC 26  
||||| ||||| |||||  
Db 32 CATGCTATGCTCTAGCTAC 12

RESULT 10

A2831249/c

LOCUS A2831249 24 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0110621R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0110621 R, DNA sequence.

ACCESSION A2831249

VERSION A2831249.1

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 24)  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10Kb

Plasmid Inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers, Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0110 row: 6 column: 21

Seq primer: CACACAGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0110621"

/clone\_lib="Mouse 10Kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of PMD42 (911473211419b1AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 6 c 5 g 4 t

ORIGIN

Query Match 60.0%; Score 15.6; DB 17; Length 24;  
Best Local Similarity 81.8%; Pred. No. 1e+04;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TGTGCATGCTTTGTGTCACAG 22

DB 22 TGTGCATGCTTTGTGTCACAG 1

RESULT 11

T90404/c

LOCUS T90404

DEFINITION y6c02.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117890 5' similar to gb:M73700 LACTOTRANSFERRIN PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION T90404

VERSION T90404.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 28)  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chappel,B., Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,N., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasik,E., Underwood,K., Wohlmann,P., Materston,R., Wilson,R. and Marra,M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 97044478

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: estewatson.wustl.edu

Insert Size: 320

High quality sequence starts: 1 High quality sequence stops: 1

Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov)

for further information. Trace considered overall poor quality

Insert Length: 320 Std Error: 0.00

Seq primer: M13Rpl

High quality sequence stop: 1.

Location/Qualifiers

1..28

/organism="Homo sapiens"

/db\_xref="GDB:486179"

/db\_xref="taxon:9606"

/clone="IMAGE:117890"

/clone\_lib="Stratagene lung (#937210)"

/sex="male"

/dev\_stage="72 years"

/lab\_host="SOL cells (kanamycin resistant)"

/note="Organ: lung; Vector: pBluescript SK-; Site\_1: EcoRI

; Site\_2: XhoI; Cloned unidirectionally. Primer: Oligo

dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR

Vector; -5' adaptor sequence: 5' GAAATCGGCACACAG 3' -3'

adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'."

BASE COUNT 8 a 9 c 6 g 5 t

ORIGIN

Query Match 58.5%; Score 15.2; DB 14; Length 28;  
Best Local Similarity 85.0%; Pred. No. 1.6e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGCTTTGGTCCAGCTAC 26

DB 28 ATGCTATGCTCTAGCTAC 9

RESULT 12

T94189 28 bp mRNA linear EST 24-MAR-1995  
LOCUS T94189/c  
DEFINITION y62h12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119207 5' similar to gb:M73700 LACTOTRANSFERRIN PRECURSOR (HUMAN);, mRNA sequence.  
ACCESSION T94189  
VERSION T94189.1  
KEYWORDS EST.  
SOURCE human.



ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 28)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B., Chissole, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, B., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Therry-Meg, J., Trevas, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)

TITLE JOURNAL MEDLINE  
97044478

COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
Insert Size: 348  
High quality sequence starts: 1 High quality sequence stops: 1  
Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality  
Insert Length: 348 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 1.  
Location/Qualifiers  
1. 28  
/organism="Homo sapiens"  
/db\_xref="GDB:487496"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:119207"  
/clone\_lib="Stratagene Lung (#937210)"  
/sex="male"  
/dev\_stage="72 years"  
/lab\_host="SOLR cells (kanamycin resistant)"  
/note="Organ: Lung; Vector: pBluescript SK-; Site: 1: EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. normal lung. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

BASE COUNT 8 a 9 c 6 g 5 t

ORIGIN

Query Match 58.5%; Score 15.2; DB 14; Length 28;  
Best Local Similarity 85.0%; Pred. No. 1.6e+04;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGCTTTGGTCCAGCTAC 26  
|||||  
1 ATGCTTTGGTCCAGCTAC 9

Db 28 ATGCTTTGGTCCAGCTAC 9

RESULT 13  
N67043 33 bp mRNA linear EST 08-MAR-1996  
LOCUS 245612.s1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone  
DEFINITION IMAGE:296014 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA  
pseudogene (HUMAN); mRNA sequence.  
ACCESSION N67043  
VERSION N67043  
KEYWORDS EST.  
SOURCE N67043.1 GI:1219168  
human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 33)  
Hillier, L., Clark, N., Dubuque, T., Elliston, G., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project

JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality  
Seq primer: m13 -40 forward  
High quality sequence stop: 1.  
Location/Qualifiers  
1. 33  
/organism="Homo sapiens"  
/db\_xref="GDB:1240935"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:296014"  
/clone\_lib="Soares fetal liver spleen INFLS"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: Liver and Spleen; Vector: p773D (Pharmacia) with a modified polylinker; Site: 1: Pac I; Site: 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer (5' AACGTGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 5 a 9 c 11 g 7 t 1 others

ORIGIN

Query Match 58.5%; Score 15.2; DB 14; Length 33;  
Best Local Similarity 81.0%; Pred. No. 1.6e+04;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CATGCTTTGGTCCAGCTAC 26  
|||||  
1 CATGCTTTGGTCCAGCTAC 21

Db 1 CATGCTTTGGTCCAGCTAC 21

RESULT 14  
AZ438336 38 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0228E19F Mouse 10kb plasmid UGCLM library Mus musculus genomic  
DEFINITION clone UGCLM0228E19 F, DNA sequence.  
ACCESSION AZ438336  
VERSION AZ438336.1 GI:10562349  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 38)  
Dunn, D., Aoyagi, A., Barber, M., Becorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D. Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0228 row: E column: 19



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 602.344 seconds  
(without alignments)  
1449.478 Million cell updates/sec

Title: US-09-964-666-11

Perfect score: 30

Sequence: 1 ATCAACCTGGCGAACATGATGTGAACCCCATC 30

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_frod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18.6	62.0	47	6	AX378746	AX378746 Sequence
2	17.8	59.3	24	6	AX183954	AX183954 Sequence
3	17.4	58.0	29	6	A84718	A84718 Sequence 11
4	17.4	58.0	47	6	AX114379	AX114379 Sequence
5	16.8	56.0	25	6	E50643	E50643 Simple dele
6	16.6	55.3	29	6	AX021753	AX021753 Sequence
7	16.6	55.3	29	6	AX025434	AX025434 Sequence
8	16.6	55.3	29	6	AX183780	AX183780 Sequence
9	16.4	54.7	39	6	AX077406	AX077406 Sequence
10	16.2	54.0	41	6	A34769	A34769 Synthetic e
11	16	53.3	34	6	A34738	A34738 Eglin seque
12	16	53.3	34	6	A34747	A34747 Modified Eg
13	15.2	50.7	31	6	AX249031	AX249031 Sequence
14	15.2	50.7	37	6	AX425081	AX425081 Sequence
15	15.2	50.7	47	6	AX114375	AX114375 Sequence
16	15.2	50.7	50	6	AX322206	AX322206 Sequence
17	15.2	50.7	41	6	AX230591	AX230591 Sequence
18	15	50.0	41	6	AX268229	AX268229 Sequence
19	15	50.0	41	6	AX268242	AX268242 Sequence
20	15	50.0	42	6	A93509	A93509 Sequence 2
21	15	50.0	48	6	A93513	A93513 Sequence 6
22	15	50.0	48	6	A93514	A93514 Sequence 7
23	14.8	49.3	26	6	AR080211	AR080211 Sequence
24	14.8	49.3	26	6	AR103647	AR103647 Sequence
25	14.6	48.7	26	6	AX190637	AX190637 Sequence
26	14.6	48.7	27	6	AX289931	AX289931 Sequence
27	14.6	48.7	29	6	AX283139	AX283139 Sequence
28	14.6	48.7	31	6	A76904	A76904 Sequence 10
29	14.6	48.7	31	6	I49720	I49720 Sequence 14
30	14.6	48.7	41	6	AX022217	AX022217 Sequence
31	14.6	48.7	41	6	AX030743	AX030743 Sequence
32	14.6	48.7	41	6	BD008658	BD008658 Stable ex
33	14.4	48.0	37	6	AX192292	AX192292 Sequence
34	14.4	47.3	19	12	AB069002	AB069002 Synthetic
35	14.2	47.3	27	6	AX268952	AX268952 Sequence
36	14.2	47.3	30	6	AX441224	AX441224 Sequence
37	14.2	47.3	34	6	AR025212	AR025212 Sequence
38	14.2	47.3	34	6	AR029059	AR029059 Sequence
39	14.2	47.3	34	6	AR110630	AR110630 Sequence
40	14.2	47.3	34	6	AX040099	AX040099 Sequence
41	14.2	47.3	37	6	AX219952	AX219952 Sequence
42	14.2	47.3	37	6	AX220037	AX220037 Sequence
43	14.2	47.3	37	6	AX425140	AX425140 Sequence
44	14.2	47.3	37	6	AX425148	AX425148 Sequence
45	14	46.7	24	6	AX446233	AX446233 Sequence

# ALIGNMENTS

RESULT 1	AX378746/c	47 bp	DNA	linear	PAT 18-MAR-2002
LOCUS	AX378746				
DEFINITION	Sequence 535 from Patent WO0206525.				
ACCESSION	AX378746				
VERSION	AX378746.1				
KEYWORDS	GT:19574599				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	1. Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	Cohen, D., Blumenfeld, M., Chumakov, I., Abderrahim, H. and Bihain, B.				
JOURNAL	Obesity associated biallelic marker maps				
	Patent: WO 0206525-A 535 24-JAN-2002;				

FEATURES	GENSET (FR)					
SOURCE	Location/Qualifiers 1..47 /organism="Homo sapiens" /db_xref="taxon:9606"					
VARIATION	/note="99-4582-359 : polymorphic base G or T" 24					
BASE COUNT	8 a      14 c      11 g      13 t      1 others					
ORIGIN						
Query Match	Best Local Similarity      62.0% ; Score 18.6; DB 6; Length 47; Matches      21; Conservative      1; Mismatches      5; Indels      0; Gaps      0;					
OY	1 ATCAACCTGGCGAACATGTTGAACCCC 27                               30 ACCATCMGTGGTAAACACGGTGAACCC 4					
RESULT 2						
LOCUS	AXI83954      24 bp      DNA					
DEFINITION	Sequence 1707 from Patent WO0142511.					
ACCESSION	AXI83954					
VERSION	AXI83954.1 GI:15135287					
KEYWORDS	human.					
SOURCE	Human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 24) Daly,M., Hudson,T.J., Lander,E.S., Roux,J. and Simionovitch,K. Ibd-related polymorphisms Patent: WO 0142511-A 1707 14-JUN-2001; WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis Biotherapeutics Corporation (CA)					
AUTHORS	Location/Qualifiers 1..24 /organism="Homo sapiens" /db_xref="taxon:9606"					
TITLE						
JOURNAL						
FEATURES						
SOURCE						
BASE COUNT	5 a      9 c      5 g      4 t      1 others					
ORIGIN						
Query Match	59.3% ; Score 17.8; DB 6; Length 24; Best Local Similarity      86.4% ; Pred.No.3.5e+03; Matches      19; Conservative      0; Mismatches      3; Indels      0; Gaps      0;					
OY	6 CCGGCCAAGCATGGTGAAACCCC 27                               2 CCTGCCCAACTGTTGTAACCCC 23					
Db						
RESULT 3						
LOCUS	AB4718      29 bp      DNA					
DEFINITION	Sequence 11 from Patent W09844152.					
ACCESSION	AB4718					
VERSION	AB4718.1 GI:6733586					
KEYWORDS	unidentified. unclassified.					
SOURCE	unclassified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 29) Farinelli,L. and Mayer,P. METHOD OF NUCLEIC ACID SEQUENCING Patent: WO 9844152-A 11 08-OCT-1998; FARINELLI LAURENT (CH); MAYER PASCAL (CH)					
AUTHORS	Location/Qualifiers 1..29 /organism="unidentified" /db_xref="taxon:32644"					
TITLE						
JOURNAL						
FEATURES						
SOURCE						
BASE COUNT	2 a      6 c      11 g      10 t					
ORIGIN						

Query Match	Similarity	58.0%	Score	17.4	DB	6	Length	29;
Best Local	Similarity	77.8%	Pred.	No. 5.3e+03;				
Matches	21; Conservative	0;	Mismatches	6;	Indels	0;	Gaps	0;
Oy	1 ATCAACCTGGCGAACATGTTGAACCCC	27						
Db	.28 ACCAGCCTTGACCACATGTGAGAACC	2						
RESULT 4	AXI14379	47 bp	DNA	linear	PAT 11-MAY-2001			
LOCUS	Sequence	48 from Patent.WO0129257.						
DEFINITION	AXI14379							
ACCESSION	AXI14379							
VERSION	AXI14379.1 GI:14031343							
KEYWORDS								
SOURCE	human.							
ORGANISM	Homo sapiens							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
REFERENCE	1 (bases 1 to 47)							
AUTHORS	SCHORK,N. and Skierczynski,B.							
TITLE	Methods of genetic cluster analysis and use thereof							
JOURNAL	Patent: WO 0129257-A 48 26-Apr-2001;							
	GENSET (FR)							
FEATURES	Location/Qualifiers							
source	1..47							
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	/db_xref="taxon:9606"							
	24							
Variation	/note="99-1602-200 : polymorphic base G or C"							
BASE COUNT	16 a 14 c 7 g 9 t 1 others							
ORIGIN								
Query Match	58.0%, Score 17.4; DB 6; Length 47;							
Best Local Similarity	77.8%; Pred.No. 5.5e+03;							
Matches	21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;							
Oy	1 ATCAACCTGGCGAACATGTTGAACCCC	27						
Db	8 ACCATCTTGGCTTAACASAGTGAACCC	34						
RESULT 5	E50643	25 bp	DNA	linear	PAT 31-JAN-2002			
LOCUS	E50643							
DEFINITION	Simple detection method of drug-metabolizing synthetase gene							
ACCESSION	E50643							
VERSION	E50643.1 GI:18629424							
KEYWORDS	JP 2001017185-A/7.							
SOURCE	unidentified.							
ORGANISM	unclassified.							
REFERENCE	1 (bases 1 to 25)							
AUTHORS	Mizugaki,M. and Hiratsuka,M.							
TITLE	Simple detection method of drug-metabolizing synthetase gene							
JOURNAL	Patent: JP 2001017185-A 7 23-JAN-2001;							
	OTSUKA PHARMACEUT CO LTD							
COMMENT	OS Unidentified							
	PN JP 2001017185-A/7							
	PD 23-JAN-2001							
	PE 10-DEC-1999 JP 1999351610							
	PR							
	PT MICHIMAO MIZUGAKI,MASAHIRO HIRATSUKA							
	PC C12N15/09,C12Q1/68,C12Q1/68,C12N15/00							
	CC							
	FH key							
	FT source							
	FT 1..25							
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	1..25							
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FEATURES	Location/Qualifiers							
source	1..25							

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BASE COUNT      6 a      7 c      6 g      6 t
ORIGIN

Query Match      56.0%; Score 16.6; DB 6; Length 25;
Best Local Similarity 90.0%; Pred. No. 9.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 TGGCGACATGCGTAACCC 27
      1 TGGCCACATGCTGAACCC 20
Db

RESULT 6
AX021753/c      AX021753      29 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION      Sequence 84 from Patent WO923221.
ACCESSION      AX021753
VERSION      AX021753.1 GI:10045009
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 29)
AUTHORS      Howell, S., Ledebuer, A.M., Frenken, L.G. and van der Logt, C.P.E.
TITLE      Multivalent antigen-binding proteins
JOURNAL      Patent: WO 923221-A 84 14-MAY-1999;
      HOWELL, STEVEN (GB); UNILEVER PLC (GB); LEDEBUER ADRIANUS MARINUS
      (NL); LOGT CORNELIS PAUL ERIK V D (NL); UNILEVER NV (NL); FRENKEN
      LEON GERARDUS JOSEPH (NL)
FEATURES
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      1..29
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      /note="linker"

BASE COUNT      5 a      8 c      8 g      8 t
ORIGIN

Query Match      55.3%; Score 16.6; DB 6; Length 29;
Best Local Similarity 82.6%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 ACCTGGCGAAGTGTGAACCC 27
      26 ACCTGGTGAACCTGGAGAACAC 4
Db

RESULT 7
AX025434/c      AX025434      29 bp      DNA      linear      PAT 16-SEP-2000
DEFINITION      Sequence 37 from Patent EP1002861.
ACCESSION      AX025434
VERSION      AX025434.1 GI:10187110
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      synthetic construct.
FEATURES      artificial sequences.
      source
      1..29
      /organism="synthetic construct"
      /db_xref="taxon:32630"
      /note="linker"

BASE COUNT      5 a      8 c      8 g      8 t
ORIGIN

Query Match      55.3%; Score 16.6; DB 6; Length 29;
Best Local Similarity 82.6%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 ACCTGGCGAAGTGTGAACCC 27
      26 ACCTGGTGAACCTGGAGAACAC 4
Db

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RESULT 8
AX183780
LOCUS      AX183780      40 bp      DNA      linear      PAT 06-AUG-2001
DEFINITION      Sequence 1533 from Patent WO0142511.
ACCESSION      AX183780
VERSION      AX183780.1 GI:15135106
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS      Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K.
TITLE      1 (bases 1 to 40)
JOURNAL      Idb-related polymorphisms
      Patent: WO 0142511-A 1533 14-JUN-2001.
      WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); ELLIPSIS
      BIOTHERAPEUTICS CORPORATION (CA)
FEATURES
      source
      1..40
      /organism="Homo sapiens"
      /db_xref="taxon:9606"

BASE COUNT      13 a      7 c      12 g      7 t      1 others
ORIGIN

Query Match      55.3%; Score 16.6; DB 6; Length 40;
Best Local Similarity 82.6%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 ATCAACCTGGCGAAGTGTGA 23
      17 ACCAGCCTGACTACATGCTGA 39
Db

RESULT 9
AX077406/c      AX077406      39 bp      DNA      linear      PAT 22-FEB-2001
DEFINITION      Sequence 19 from Patent WO0107640.
ACCESSION      AX077406
VERSION      AX077406.1 GI:13121956
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 39)
AUTHORS      Gill, P.T., Hussain, J.T. and Long, A.T.
TITLE      Improvements in and relating to analysis of dna
JOURNAL      Patent: WO 0107640-A 19 01-FEB-2001;
      The Secretary of State for the Home Department (GB)
FEATURES
      source
      1..39
      /organism="synthetic construct"
      /db_xref="taxon:32630"
      /note="A human Gc forward primer attached to an artificial
      universal primer tag to detect a SNP polymorphism at
      GcIs/IIf, page 48."

BASE COUNT      5 a      11 c      11 g      12 t
ORIGIN

Query Match      54.7%; Score 16.4; DB 6; Length 39;
Best Local Similarity 76.9%; Pred. No. 1.5e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      5 ACCTGGCGAAGTGTGAACCCATC 30
      36 AACTGGCAAGCTGTGAAGACATC 11
Db

RESULT 10
A34769
LOCUS      A34769      41 bp      DNA      linear      PAT 03-JUL-2002
DEFINITION      Synthetic eglin gene duplex.

```

ACCESSION	A34769
VERSION	A34769.1
KEYWORDS	GI:21694261
SOURCE	.
ORGANISM	synthetic construct.
REFERENCE	artificial construct.
AUTHORS	1 (bases 1 to 41)
TITLE	Ritz,H., Liersch,M., Sieber,P., Rittel,W., Meyer,F., Seemüller,U., Fritz,H., Maerki,W. and Alkan,S. Process for the preparation of protease inhibitors Patent: EP 0146785-A 43 03-JUL-1985; CIBA-GEIGY AG; PLANTORGAN WERK Heinrich G.E. Christensen KG
FEATURES	location/Qualifiers
SOURCE	1..41
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	/db_xref="taxon:32630"
BASE COUNT	15 a 10 c 8 g 8 t
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	Best Local Similarity	72.4%	Pred. NO.1.9e+04;		
	Matches	21;	Conservative	0;	Mismatches 8; Indels 0;
Qy	1 ATCAACCTGGCGAACAATGTCGAACCCCAT	29			
Db	11 ACCAACATGCGAGAACATGTTAAACAACCT	39			

RESULT	11
A34738	
LOCUS	A34738
DEFINITION	Eglin sequence.
ACCESSION	A34738
VERSION	A34738.1
KEYWORDS	GI:1568271
SOURCE	.
ORGANISM	unidentified. unclassified.
REFERENCE	1 (bases 1 to 34) Rink,H., Liersch,M., Sieber,P., RitteI,W., Meyer,F., Seemuller,U., Fritz,H., MaerkI,W. and Alkan,S. Process for the preparation of protease inhibitors Patent: EP 0146785-A 12 03-JUL-1985; CIBA-GEIGY AG; PLANTORGAN WERK Heinrich G.E. Christensen KG
TITLE	
JOURNAL	
FEATURES	
source	location/Qualifiers 1..34 /organism="unidentified" /db_xref="taxon:32644"
BASE COUNT	12 a 9 c 7 g 6 t
ORIGIN	

Query	1	ATCAACCTGGCGAACATGCTGAAC	24
	.		
	11	ACCAACATGGCGAACATGCTTAAC	34
Db			
	11	ACCAACATGGCGAACATGCTTAAC	34
Matches	19;	Conservative	0;
		Mismatches	5;
		Indels	0;
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Query Match	53.3%;	Score	16;
		DB	6;
		Length	34;
Best Local Similarity	79.2%;	Pred. No.	2.3e+04;
Matches	19;	Conservative	0;
		Mismatches	5;
		Indels	0;
		Gaps	0;

RESULT 12				
A34747/c				
LOCUS	A34747	34 bp	DNA	linear
DEFINITION	Modified Eg1n C sequence.			
ACCESSION	A34747			
VERSION	A34747.1	GI:21694241		
KEYWORDS				
SOURCE	unidentified.			
ORGANISM	unclassified.			
	unclassified.			
REFERENCE	1 (bases 1 to 34)			
AUTHORS	Rank,H., Liersch,M., Sieber,P., Ritte,W., Meyer,F., Seemuller,U., Filtz,H., Maerkl,W. and Alkan,S.			

TITLE	Process for the preparation of protease inhibitors									
JOURNAL	Patent: EP 0146785-A 21-03-JUL-1985									
FEATURES	CIBA-GEIGY AG; PLANTORGAN WERK Heinrich G.E. Christensen KG									
SOURCE	Location/Qualifiers 1..34									
BASE COUNT	/organism="unidentified" /db_xref="taxon:32644"									
ORIGIN	6 a 7 c 9 g 12 t									
Query Match	53.3%; Score 16; DB 6; Length 34;									
Best Local Similarity	79.2%; Pred. No. 2.3e+04;									
Matches	19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;									
QY	1 ATCAACCTGGGACACATGCTGAAC 24									
Db	24 ACCACACATGGCGACACATGGTTAAC 1									

RESULT	13
LOCUS	AX249031/c
DEFINITION	AX249031 31 bp DNA linear PAT 28-SEP-2001
ACCESSION	Sequence 1110 from Patent WO016680.
VERSION	AX249031
KEYWORDS	AX249031.1 GI:15863654
SOURCE	.
ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 31)
AUTHORS	Cargill,M., Ireland,J.S. and lander,E.S.
TITLE	Human single nucleotide polymorphisms
JOURNAL	Patent: WO 0166800-A 1110 13-SEP-2001;
FEATURES	WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) Location/Qualifiers 1..31 /organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	6 a 11 c 4 g 9 t 1 others
ORIGIN	

Query	8	TGGCGACATGCTGACCCCAT	29
	111	1111111111111111	1111
Db	25	TGGTGTCATGCGTGAAGCCCAT	4

RESULT 14					
AX425081/c					
LOCUS	AX425081	37 bp	mRNA	linear	PAT 18-JUN-2002
DEFINITION	Sequence 3417 from Patent WO0188124.				
ACCESSION	AX425081				
VERSION	AX425081.1	GI:21528463			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS	Jarvis,T., von Carlowitz,I., Mcswigen,J.A., McLaughlin,F.C. and Randl,A.M.				
TITLE	Method and reagent for the inhibition of eeg				
JOURNAL	Patent: WO 0188124-A 3417 22-NOV-2001;				
FEATURES	<p> RIBOZYME PHARMACEUTICALS, INC. (US) ; GLANO GROUP LIMITED (GB)  location/Qualifiers  1..37  /organism="synthetic construct"  /db_xref="taxon:32630"  /note="Enzymatic Nucleic Acid" </p>				
source					
BASE COUNT	7 a	8 c	10 g	12 t	



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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.4	71.3	29	21	AAA03983
2	20.6	68.7	41	24	ABA01400
3	20.6	68.7	41	24	ABA01401
4	19.2	64.0	33	24	AAAS1589
5	19	63.3	41	24	ABLA9775
6	19	63.3	41	24	ABLA9776
7	19	63.3	47	21	AAZ65526
8	19	63.3	49	22	AAK65537
9	19	63.3	49	22	AAI62905

C	10	18.6	62.0	47	24	ABK41287	Human USP2 gene bi
C	11	18.4	61.3	29	21	AAA04485	Polymorphic fragme
C	12	18.2	60.7	33	24	ABK12114	Human EHD 9.57 pro
C	13	18.2	60.7	33	24	ABK14174	Insulin like growt
C	14	18.2	60.7	34	22	AAH27605	Human II aminoacyl
C	15	18	60.0	29	21	AAA04312	Polymorphic fragme
C	16	17.8	59.3	24	22	AAH91382	Human inflammatory
C	17	17.8	59.3	33	24	ABA01398	Human NF-E2-associ
C	18	17.6	58.7	41	24	ABA94080	Human multi-copper
C	19	17.6	58.7	41	24	ABA94081	Human multi-copper
C	20	17.4	58.0	33	22	AAI65108	Human hypoxia-indu
C	21	17.4	58.0	41	24	AAI43826	Human oncogene pro
C	22	17.4	58.0	41	24	AAI43827	Human oncogene pro
C	23	17.4	58.0	41	24	ABA96812	Human uteroglobin
C	24	17.4	58.0	41	24	ABA96813	Human uteroglobin
C	25	17.4	58.0	47	21	AAZ66299	Human map-related
C	26	17.4	58.0	47	22	AAH89248	Sample member clus
C	27	17.4	58.0	50	22	AAI28723	Human SNP oligonuc
C	28	17.2	57.3	29	21	AAA04311	Polymorphic fragme
C	29	17.2	57.3	33	24	ABR84112	Human protein 11.1
C	30	17	56.7	29	21	AAA04503	Polymorphic fragme
C	31	16.8	56.0	25	22	AAH84351	Human CYP2C18i PCR
C	32	16.6	55.3	24	24	ABA02134	Human zinc ion tra
C	33	16.6	55.3	29	21	AAH91207	Synthetic oligonuc
C	34	16.6	55.3	40	22	AAH91207	Human inflammatory
C	35	16.4	54.7	39	22	AAH74239	DNA analysis metho
C	36	16.4	54.7	41	24	ABH77547	Human red blood ce
C	37	16.2	54.0	22	21	ABD00662	Synthetic oligonuc
C	38	16.2	54.0	33	24	ABL49773	Human tyrosinase 1
C	39	16	53.3	33	24	ABL61326	Human pur-alpha 13
C	40	16	53.3	41	24	ABK47938	Corticotrophin rel
C	41	16	53.3	41	24	ABK47939	Corticotrophin rel
C	42	15.6	52.0	31	22	AAI30622	Human single nucle
C	43	15.6	52.0	33	24	ABK14188	Human splicing fac
C	44	15.6	52.0	33	24	ABA02347	Human pax protein
C	45	15.6	52.0	34	22	AAH46543	DNA polymerase 17

## ALIGNMENTS

RESULT 1	AAA03983	standard: DNA; 29 BP.
ID	AAA03983	
AC	AAA03983:	
XX		
DT	22-MAY-2000	(first entry)
XX		
DE		Polymorphic fragment of hypertension associated gene APOC3.
XX		
KW		Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus;
KW		Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KW		Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
KW		polycystic kidney disease; von Willebrand's disease; forensic; human;
KW		tubercous sclerosis; hereditary hemorrhagica telangiectasia;
KW		familial colonic polyposis; osteogenesis imperfecta; porphyria;
KW		Ehlers-Danlos syndrome; ss.
XX		
OS	Homo sapiens.	
XX		
PN	EP955382-A2.	
XX		
PD	10-NOV-1999.	
XX		
PF	07-MAY-1999.	99EP-0250150.
XX		
PR	07-MAY-1998:	98US-0084641.
XX		
PR	03-MAY-1999:	99US-0304232.
XX		
PA	(AFV-) AFFYMETRIX INC.	
XX		
PA	(UYCA-) UNIV CASE WESTERN RESERVE.	
XX		

P1 Fan JB, Chakravarti A, Haluska MK;  
XX  
XX  
DR WPI: 2000-107928/10.  
XX  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
PT hypertension -  
XX  
PS Claim 1; Page 22: 53pp: English

The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimens customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension diagnostic assays. Where the polymorphisms have strong correlation with hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. aqumaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial acrotic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals.

5Q, Sequence 29 BP; 9 A; 11 C; 5 G; 3 T; 1 other;

Query Match	71.3%	Score 21.4	DB 21	Length 29	.
Best Local Similarity	88.0%	Pred. No. 14			
Matches 22	Conservative 1	Mismatches 2	Indels 0	Gaps 0	

QY	3	CAACCTGGCGAACATGTTGAACCCC	27
		:	
Db	1	CAACCTGGCCAACACAYGGTGAACCC	25

RESULT 2  
ABA01400/c  
ID ABA01400 standard; DNA; 41 BP.

DT 31-JAN-2002 . (first entry)

DE Human NF-E2-associated factor 13 probe #1.

KM Human; NF-E2-associated factor 13; cytosolic; virucidal,  
immunomodulatory; antiinflammatory; haemostatic; gene therapy; tumour  
hemopathy; HIV infection; immunological disease; inflammation;  
developmental disorder; probe; ss.

OS Homo sapiens.

PN W0200175024-A2.

PD 11-OCT-2001

PF 19-MAR-2001; 2001WO-CN00368.

PR 22-MAR-2000; 2000CN-0115024

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR 'WPI; 2002-025846/03.

PT	Human NF-E2-associated factor 13 and encoded polynucleotide, applicable
PT	in diagnosis and treatment of e.g. malignant tumor, hemopathy, HIV

PT infection, immunological diseases and inflammation  
XX  
PS  
Example 6; Page 15; 34pp; Chinese.

CC The present invention relates to human NF-E2-associated factor 13 (see  
CC AAM55244). The factor and its coding sequence are useful in the diagnosis  
CC and treatment of malignant tumours, haemophagy, HIV infection,  
CC immunological diseases, various inflammations and developmental  
CC disorders. The present sequence is a probe, which was used in an  
CC example from the present invention.

Sequence 41 BP; 7 A; 11 C; 13 G; 10 T; 0 other;

Query Match	68.7%	Score 20.6	DB 24	Length 41
Best Local Similarity	85.2%	Pred. No. 30		
Matches 23, Conservative	0	Mismatches 4	Indels 0	Gaps 0

QY	1	ATCAACCTGGCGAACATGGTGAACCCC	27
Db	29	ACCAGCCTGGCGAACATGGTGAACCCC	3

RESULT 3  
ABA01401/c  
ID ABA01401 standard; DNA; 41 BP.

AC ABA01401;

DT 31-JAN-2002 (first entry)

Human NF-E2-associated factor 13 probe #2.

KM Human; NF-E2-associated factor 13; cytosol; viral; viral;  
KM Immunomodulatory; anti-inflammatory; haemostatic; gene therapy; tumour;  
KW HIV infection; immunological disease; inflammation;  
KW developmental disorder; probe; ss.

OS Homo sapiens.

PN WO200175024-A2.

PD 11-OCT-2001.

PF 19-MAR-2001; 2001WO-CN00368.

PR 22-MAR-2000; 2000CN-0115024

PA (BLOW-) BLOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-025846/03.

PT Human NF- $\kappa$ B-associated factor 13 and encoded polynucleotide, applicable  
PT in diagnosis and treatment of e.g. malignant tumor, hemopathy, HIV  
PT infection, immunological diseases and inflammation

PS Example 6; Page 15; 34pp; Chinese.

CC The present invention relates to human NF-E2-associated factor 13 (see  
CC \* [MM552544](#)). The factor and its coding sequence are useful in the diagnosis  
CC and treatment of malignant tumours, haemopathy, HIV infection,  
CC immunological diseases, various inflammations and developmental  
CC disorders. The present sequence is a probe, which was used in an  
CC example from the present invention.

Sequence 41 BP; 7 A; 11 C; 13 G; 10 T; 0 other;

Query Match	68.7%;	Score 20.6;	DB 24;	Length 41;
-------------	--------	-------------	--------	------------

Best Local Similarity 85.2%; Pred. No. 30;  
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0.

QY 1 ATCAACCTGGCGACATGCTGAACCC 27

DB 29 ACCAGCTGGCCACATGCTGAACCC 3

RESULT 4

ID AAS15589 standard; DNA; 33 BP.

AC AAS15589;

DT 14-FEB-2002 (first entry)

DE Human DNA mismatch repair protein 10, PCR primer #2.

XX Human; DNA mismatch repair protein 10; cytostatic; virucidal;

KW immunomodulatory; anti-inflammatory; haemostatic; anti-HIV; inflammation;

KM human immunodeficiency virus; malignancy; haemopathy; infection;

XX immunological disease; PCR primer; ss.

OS Homo sapiens.

XX WO200175100-A1.

PN 11-OCT-2001.

XX 19-MAR-2001; 2001WO-CN00337.

XX 22-MAR-2000; 2000CN-0115057.

XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-025860/03.

XX New human DNA mismatch repair protein 10 for diagnosing and treating

XX malignancy, haemopathy, human immunodeficiency virus infection,

XX immunological diseases and inflammation

XX Example 4; Page 13; 36pp; Chinese.

XX The invention relates to an isolated polypeptide of human DNA mismatch

XX repair protein 10. The polypeptide can be used for screening mimics,

XX agonists, antagonists or inhibitors, or in peptide fingerprinting

XX identification. The polynucleotide can be used as primers for nucleic

XX acid amplification reactions, as probes for hybridisation reactions, or

XX in producing gene chips or microarrays. Drug compositions, which contain

XX the polypeptide, polynucleotide, mimics, agonists, antagonists,

XX inhibitors and their preparations, can be used treatment and

XX diagnosis of diseases relating to the polypeptide. In particular, the

XX polypeptide and encoded polynucleotide are applicable in diagnosis and

XX treatment of malignancy, haemopathy, human immunodeficiency virus (HIV)

XX infection, immunological diseases and various inflammations. The

XX present sequence represents PCR primer #2 used to amplify human DNA

XX mismatch repair protein 10.

XX Sequence 33 BP; 9 A; 10 C; 8 G; 6 T; 0 other;

XX Query Match 64.0%; Score 19.2; DB 24; Length 33;

XX Best Local Similarity 87.5%; Pred. No. 1.1e+02;

XX Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX 2 TCACCTGCGGACATGCTGAAC 25

XX 10 TCAGCTGGCCACATGCTGAAC 33

RESULT 5

ID ABL49775/C

XX ABL49775 standard; DNA; 41 BP.

XX ABL49775;

DT 29-MAY-2002 (first entry)

XX Human tyrosinase 10.34 probe 1 SEQ ID NO:8.

XX Human; tyrosinase; enzyme; human immunodeficiency virus infection;

KW HIV infection; cancer; probe; ss.

XX Homo sapiens.

XX CN1325972-A.

XX 12-DEC-2001.

XX 31-MAY-2000; 2000CN-0116261.

XX 31-MAY-2000; 2000CN-0116261.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-196693/26.

XX New polypeptide-tyrosinase 10.34 for treating diseases such as cancer

XX and human immunodeficiency virus infection

XX Example 6; Page 19 (Disclosure); 32pp; Chinese.

XX The present invention describes human tyrosinase 10.34 (I). The present

XX invention also described a method for preparing (I) using DNA

XX recombination techniques. (I) and the polynucleotide encoding it can

XX be used in the treatment of diseases such as cancer and human

XX immunodeficiency virus (HIV) infection. The present sequence represents

XX a probe for human tyrosinase 10.34, which is used in an example from

XX the present invention.

XX Sequence 41 BP; 5 A; 12 C; 13 G; 11 T; 0 other;

XX Query Match 63.3%; Score 19; DB 24; Length 41;

XX Best Local Similarity 81.5%; Pred. No. 1.4e+02;

XX Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

XX 1 ATCAACCTGCGGACATGCTGAACCC 27

XX 29 ACCAGCCGCGCAACTGTGAACCC 3

XX ABL49776 standard; DNA; 41 BP.

XX ABL49776;

XX 29-MAY-2002 (first entry)

XX Human tyrosinase 10.34 probe 2 SEQ ID NO:9.

XX Human; tyrosinase; enzyme; human immunodeficiency virus infection;

KW HIV infection; cancer; probe; ss.

XX Homo sapiens.

XX CN1325972-A.

XX 12-DEC-2001.

XX 31-MAY-2000; 2000CN-0116261.

XX 31-MAY-2000; 2000CN-0116261.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

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XX WP1. 2002-196693/26.
DR
XX New polypeptide-tyrosinase 10.34 for treating diseases such as cancer
XX and human immunodeficiency virus infection -
XX
XX
XX Example 6; Page 19 (Disclosure); 32pp; Chinese.
XX
XX The present invention describes human tyrosinase 10.34 (1). The present
XX invention also described a method for preparing (1) using DNA
XX recombination techniques. (1) and the polynucleotide encoding it can
XX be used in the treatment of diseases such as cancer and human
XX immunodeficiency virus (HIV) infection. The present sequence represents
XX a probe for human tyrosinase 10.34, which is used in an example from
XX the present invention.
XX
XX Sequence 41 BP; 5 A; 12 C; 13 G; 11 T; 0 other;
XX
XX Query Match 63.3%; Score 19; DB 24; Length 41;
XX Best Local Similarity 81.5%; Pred. No. 1.4e+02;
XX Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 ATCAACCTGGCCGACACATGTGTAACCCC 27
XX | | | | | | | | | | | | | | | | |
XX 29 ACCAGCCCGGCCACACATGTGTAACCCC 3
XX
XX RESULT 7
XX AAZ69526/c
XX ID AAZ69526 standard; DNA; 47 BP.
XX AC
XX AAZ69526;
XX
XX 10-SEP-2001 (first entry)
XX
XX Human map-related diallelic marker SEQ ID NO:3882.
XX
XX Human genome: diallelic marker: high density disequilibrium map;
XX genomic map; haplotype; phenotype; polymorphic base; genotyping;
XX haplotyping; hybridisation; identification; characterisation;
XX diagnosis; single nucleotide polymorphism; SNP; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Variation replace(24,T)
XX FT /tag=a
XX FT /standard_name="single nucleotide polymorphism"
XX
XX WO954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB00822.
XX
XX 21-APR-1998; 98US-0082614.
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI: 2000-013267/01.
XX
XX Novel diallelic markers used to construct a high density disequilibrium
XX map of the human genome -
XX
XX Claim 3; Page 1058; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human diallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the diallelic markers. The diallelic markers of the

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	CC	invention have a variety of uses they can be used for high density
	CC	mapping of the human genome, and in complex association studies and
	CC	haplotyping studies which are useful in determining the genetic basis
	CC	for disease states. Compositions and methods of the invention can also
	CC	be useful for the identification of the targets for the development of
	CC	pharmaceutical agents and diagnostic methods, as well as the
	CC	characterisation of the differential efficacious responses to and side
	CC	effects from pharmaceutical agents acting on a disease as well as other
	CC	treatment.
	CC	N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
	CC	and 3367, are not actually given a sequence in the Sequence Listing
	CC	from the present invention.
	XX	
SO		Sequence 47 BP; 8 A; 14 C; 12 G; 13 T; 0 other;
DQ		
DQ	1	ATCAACTGGCGACATGCTAACC CC 27
DQ	1	
DQ	30	ACCATCGTGCTAACACGTTAAACC C 4
RESULT 8		
ID	AAK65537/c	
AC	AAK65537 standard; DNA; 49 BP.	
XX	AAK65537;	
DT	06-NOV-2001 - (first entry)	
XX		
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20349.	
XX		
KW	Human; Immune; haematopoietic; immune/haematopoietic antigen; cancer;	
KW	Cytostatic; gene therapy; vaccine; metastasis; ds.	
OS	Homo sapiens.	
XX		
PN	WO200157182-A2.	
PD	09-AUG-2001.	
PF	17-JAN-2001; 2001WO-US01354.	
XX		
PR	31-JAN-2000; 2000US-0179065.	
PR	04-FEB-2000; 2000US-0180628.	
PR	24-FEB-2000; 2000US-0184664.	
PR	02-MAR-2000; 2000US-0186350.	
PR	16-MAR-2000; 2000US-0189874.	
PR	17-MAR-2000; 2000US-0190076.	
PR	18-APR-2000; 2000US-0198123.	
PR	19-MAY-2000; 2000US-0205515.	
PR	07-JUN-2000; 2000US-0209467.	
PR	28-JUN-2000; 2000US-0214886.	
PR	30-JUN-2000; 2000US-0215135.	
PR	07-JUL-2000; 2000US-0216647.	
PR	11-JUL-2000; 2000US-0216880.	
PR	11-JUL-2000; 2000US-0217487.	
PR	11-JUL-2000; 2000US-0217496.	
PR	14-JUL-2000; 2000US-0218290.	
PR	26-JUL-2000; 2000US-0220965.	
PR	26-JUL-2000; 2000US-0220964.	
PR	14-AUG-2000; 2000US-0224518.	
PR	14-AUG-2000; 2000US-0224519.	
PR	14-AUG-2000; 2000US-0225213.	
PR	14-AUG-2000; 2000US-0225214.	
PR	14-AUG-2000; 2000US-0225266.	
PR	14-AUG-2000; 2000US-0225267.	
PR	14-AUG-2000; 2000US-0225268.	
PR	14-AUG-2000; 2000US-0225270.	
PR	14-AUG-2000; 2000US-0225447.	
PR	14-AUG-2000; 2000US-0225757.	

PR 14-AUG-2000; 2000US-0225758.  
 PR 14-AUG-2000; 2000US-0225759.  
 PR 18-AUG-2000; 2000US-0226579.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226686.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231242.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234397.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246539.

PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251997.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-483426/52.  
 DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating cancers and  
 PT metastasis.  
 XX  
 PS Disclosure; SEQ ID NO 20349; 3071pp + Sequence Listing; English.  
 XX  
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
 CC activity, and can be used in gene therapy and vaccine production. (I),  
 CC proteins and polynucleotides may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate (I) expression. For  
 CC example, they may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of (I) by expressing inactive proteins or to  
 CC supplement the patients own production of (I). Additionally, (I)  
 CC polynucleotides may be used to produce the secreted (I), by inserting  
 CC the nucleic acids into a host cell and culturing the cell to express the  
 CC protein. (I) proteins and polynucleotides may be used to prevent,  
 CC diagnose and treat immune/hematopoietic-related diseases, especially  
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
 CC to AAK87694 represent human immune/hematopoietic antigen genomic  
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
 CC represent sequences used in the exemplification of the present invention.  
 XX  
 SO Sequence 49 BP; 11 A; 12 C; 13 G; 13 T; 0 other;  
 Query Match 63.3%; Score 19; DB 22; Length 49;  
 Best Local Similarity 81.5%; Pred. No. 1,4e+02;  
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 1 ATCAACCTGGCCACATGATGAAACCC 27

DB	34	ACCATCCTGGCTAAATGCTGAACCC	8
RESULT	9		
ID	AAI62905		
XX	AAI62905 standard; DNA; 49 BP.		
XX	AAI62905;		
DT	22-OCT-2001 (first entry)		
DE	Human genomic DNA SEQ ID NO 233.		
XX			
KW	Human; noctropic; neuroprotective; cytosolic; dermatological; virucide;		
KW	immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;		
KW	antiparkinsonian; antischizol; antianemic; antiarthritic; cancer;		
KW	antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;		
KW	antidiabetic; antidiabetic; antitumor; anticonvulsant; antifungal;		
KW	antiparasitic; cardiac; immune disorder; cardiovascular disorder;		
KW	neurological disease; infection; nephrotropic; gene therapy; vaccine;		
ds.			
OS	Homo sapiens.		
XX			
PN	WO200155449-A1.		
PD	02-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US01346.		
XX			
PR	31-JAN-2000; 2000US-0179065.		
PR	04-FEB-2000; 2000US-0180628.		
PR	19-MAY-2000; 2000US-0205515.		
PR	07-JUL-2000; 2000US-0216880.		
PR	14-AUG-2000; 2000US-0218290.		
PR	14-AUG-2000; 2000US-0225447.		
PR	01-SEP-2000; 2000US-0229343.		
PR	06-SEP-2000; 2000US-0230437.		
PR	08-SEP-2000; 2000US-0231243.		
PR	25-SEP-2000; 2000US-0234997.		
PR	29-SEP-2000; 2000US-0236367.		
PR	13-OCT-2000; 2000US-0239937.		
PR	08-NOV-2000; 2000US-0246476.		
PR	08-NOV-2000; 2000US-0246477.		
PR	08-NOV-2000; 2000US-0246525.		
PR	08-NOV-2000; 2000US-0246526.		
PR	08-NOV-2000; 2000US-0246528.		
PR	17-NOV-2000; 2000US-0249210.		
PR	17-NOV-2000; 2000US-0249211.		
PR	17-NOV-2000; 2000US-0249214.		
PR	17-NOV-2000; 2000US-0249215.		
PR	01-DEC-2000; 2000US-0250160.		
PR	01-DEC-2000; 2000US-0250391.		
PR	05-DEC-2000; 2000US-0251030.		
PR	05-DEC-2000; 2000US-0251988.		
PR	05-DEC-2000; 2000US-0256719.		
PR	06-DEC-2000; 2000US-0251479.		
PR	08-DEC-2000; 2000US-0251989.		
PR	08-DEC-2000; 2000US-0251990.		
PR	11-DEC-2000; 2000US-0254097.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Rosen CA, Barash SC, Ruben SM;		
XX			
DR	WPI; 2001-476225/51.		
XX			
PT	Novel plasma membrane associated proteins useful for diagnosing,		
PT	treating, preventing and/or prognosing disorders related to the		
PT	proteins, including cancer, immune response and neuronal disorders		
XX			
XX	Example 2; SEQ ID NO 233; 532pp + Sequence Listing; English.		

xx	The invention relates to novel genes (AA162752-AA162961) and proteins (AAW42347-AAW42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
cc	The nucleic acids, proteins, antibodies and (ant)isomers are useful in the diagnosis, treatment and prevention of:
cc	(a) cancer e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
cc	(b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias;
cc	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
cc	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
cc	
xx	
SQ	Sequence 49 BP; 13 A; 13 C; 12 G; 11 T; 0 other:
Query Match	63.3%; Score 19; DB 22; Length 49;
Best Local Similarity	81.5%; Pred. No. 1.4e+02;
Matches 22: Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
OY	1 ATCAACCTGGCGAACATGCTGAACCC 27                              DB      16 ACCATCCTGGCTAAAGTGTGAACCC 42

RESULT 10  
ABK41287/c  
ID ABK41287 standard; DNA: 47 BP.  
XX  
XX  
ABK41287:  
XX  
XX  
21-MAY-2002 (first entry)  
XX  
XX  
Human USF2 gene biallelic marker.  
XX  
XX  
Human; obesity associated biallelic marker; ds; LSR; USF2;  
XX  
XX  
drug response; hyperuricaemia; digestive pathology; hypertension; cancer  
XX  
XX  
hepatic function disorder; cardiovascular disease; hyperlipidaemia;  
XX  
XX  
insulin disorder; atheromatous disease; cardiac insufficiency; obesity.  
XX  
XX  
Homo sapiens.  
XX  
XX  
W0200206525-A2.  
XX  
XX  
24-JAN-2002.  
XX  
XX  
28-JUN-2001; 2001WO-1B01477.  
XX  
XX  
18-JUL-2000; 2000US-219704P.  
XX  
XX  
(GEST) GENSET.  
XX  
XX  
Cohen D, Blumenfeld M, Chumakov I, Abderrahim H, Bihain B;  
XX  
XX  
WPI; 2002-155043/20.  
XX  
XX  
Set of novel map-related biallelic markers, preferably located on  
XX  
XX  
PT obesity disorder-associated chromosomal regions on chromosomes 3, 10  
XX  
XX  
and 19, useful, for e.g. detecting statistical correlations between  
XX  
XX  
marker allele and a phenotype -  
XX  
XX  
Example 23: Page 302; 311pp; English.



Dd		31 ACCAGCCTGGCCACATGTTGAA	9
xx	RESULT 13		
xx	ABK14174/c		
ID	ABK14174 standard; DNA:	33 BP.	
xx			
xx	ABK14174;		
xx			
DT	21-MAY-2002 (first entry)		
xx			
DE	Insulin like growth factor binding protein 11.88 cDNA PCR primer #2.		
xx			
KW	Insulin like growth factor binding protein 11.88; primer: ss; cytoslatic;		
KM	embryo development dysmorphia; malignant tumour; gene therapy; cancer;		
xx	PCR.		
xx			
OS	Unidentified.		
xx			
PN	WO200212493-A1.		
xx			
PD	14-FEB-2002.		
xx			
FE	11-JUN-2001; 2001WO-CN00951.		
xx			
PR	14-JUN-2000; 2000CN-0116491.		
xx			
PA	(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.		
PI	Mao Y, Xie Y;		
DR	WPI: 2002-172159/22.		
PT	Insulin like growth factor binding protein 11.88 and encoding		
xx	polynucleotide, used in diagnosis and treatment of malignant tumours -		
PS	Example 4; Page 13; 38pp; Chinese.		
xx			
CC	The invention relates to an insulin like growth factor binding protein		
CC	11.88 and the DNA sequence encoding the polypeptide. The DNA and protein		
CC	are used in diagnosis and treatment of malignant tumour and dysmorphia of		
CC	development of an embryo. This sequence represents a PCR primer used for		
CC	cloning of cDNA which encodes the insulin like growth factor binding		
CC	protein 11.88 of the invention.		
xx			
SQ	Sequence 33 BP; 5 A; 11 C; 8 G; 9 T; 0 other;		
	Query Match	60.7%; Score 18.2; DB 24;	
	Best Local Similarity	87.0%; Pred. No. 2.ge+02;	
	Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
OY	1 ATCAACTGCGGAACATGTGTA 23		
	I I I I I I I I I I I I I I I I		
Db	31 ACCAGCCTGGCCACATGTTGAA 9		
RESULT 14			
ID	AAH27605/c		
ID	AAH27605 standard; DNA:	34 BP.	
xx			
AC	AAH27605;		
xx			
DT	31-AUG-2001 (first entry)		
xx			
DE	Human II aminoacyl-tRNA synthetase 9 PCR primer 4.		
xx			
KW	Human; II aminoacyl-tRNA synthetase 9; cytoslatic; antiviral;		
KM	immunomodulatory; antiinflammatory; cancer; haemopathy;		
KW	human immunodeficiency virus; HIV; infection; immunological disease;		
xx	inflammatory disease; PCR primer; ss.		
xx			
OS	Homo sapiens.		
xx			

XX	PD	07-JUN-2001.
XX	PF	27-NOV-2000; 200OWO-CN00512.
XX	PR	30-NOV-1999; 99CN-0124170.
XX	PA	(BIOR-) BIORAD GENE DEV LTD SHANGHAI.
XX	PI	Mao Y, Xie Y;
XX	DR	WPI; 2001-374843/39.
XX	PT	Human II aminoacyl-tRNA synthase 9 and encoded polynucleotide, useful in diagnosis and treatment of malignant tumor, hemopathy, HIV
XX	PS	Infection, immunological diseases and various inflammation
XX	PS	Example 4; Page 13; 38pp; Chinese.
CC	CC	The invention relates to an isolated polypeptide of human II
CC	CC	aminoacyl-tRNA synthase 9. The polypeptide comprises the 86 amino
CC	CC	acid sequence defined in the specification, or its fragment, analogue
CC	CC	or derivative. The polypeptide and the polynucleotide encoding it are
CC	CC	useful in the diagnosis and treatment of malignant tumours, hemopathy,
CC	CC	HIV infection, immunological diseases and various inflammatory diseases.
CC	CC	The polynucleotide is useful as a primer for nucleic acid amplification
CC	CC	reactions or as a probe for hybridisation reactions, or in producing gene
CC	CC	chips or microarrays. The polypeptide is useful for screening mimics,
CC	CC	agonists, antagonists or inhibitors, or for use in peptide fingerprinting
CC	CC	identification. The present sequence is a primer which was used to
CC	CC	amplify the polynucleotide encoding the polypeptide of the invention.
SQ		Sequence 34 BP; 6 A; 11 C; 7 G; 10 T; 0 other:
QY		Query Match                  60.7%; Score 18.2; DB 22; Length 34; Best Local Similarity        87.0%; Pred. No. 2.9e+02; Matches      20; Conservative     0; Mismatches     3; Indels        0; Gaps        0
Db		1 ATCAACCTGGCGAACATGGTGA 23                             31 ACCAGCCTGGCTAACAATGTGTA 9
RESULT 15		
ID	AAA04312/c	
AC	AAA04312 standard; DNA; 29 BP.	
DT	22-MAY-2000 (first entry)	
DE	Polymorphic fragment of hypertension associated gene GLUT4.	
KM	Polyomorphism: hypertension; agammaglobulinemia; diabetes insipidus;	
KM	Iscach-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;	
KM	Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;	
KM	polycystic kidney disease; von Willebrand's disease; forensic: human;	
KM	tubercous sclerosis; hereditary hemorrhagica telangiectasia;	
KM	familial colonic polyposis; osteogenesis imperfecta; porphyria;	
KM	Ehlers-Danlos syndrome; ss.	
OS	Homo sapiens.	
PN	EP955382-A2.	
PD	10-NOV-1999.	
PE	07-MAY-1999; 99EP-0250150.	
PR	07-MAY-1998; 98US-0084641.	
PR	03-MAY-1999; 99US-0304232.	



PA (AFY-) AFFYMETRIX INC.  
PA (UYCA-) UNIV CASE WESTERN RESERVE.

XX  
XX  
PI Fan JB, Chakravarti A, Haluska MK;  
XX

DR WPI: 2000-107928/10.

XX  
XX  
PT Novel nucleic acids containing polymorphisms used in the diagnosis of  
XX hypertension -

PS Claim 1; Page 32; 53pp; English.

XX  
XX  
CC The invention provides polymorphic fragments of genes associated with  
CC hypertension. The nucleic acids including the polymorphic sites can be  
CC used as probes or primers for expressing variant proteins. Detection of  
CC the polymorphisms is useful in designing prophylactic and therapeutic  
CC regimes customized to underlying abnormalities. The polymorphisms can be  
CC used for association studies for hypertension, and in hypertension  
CC diagnostic assays. Where the polymorphisms have strong correlation with  
CC hypertension, within a gene, they are likely to have a causative role in  
CC hypertension. This information can be used to find the precise role of a  
CC polymorphism in the disease, and this can be used to identify potential  
CC drugs which combat the disease. The polymorphisms can be tested for  
CC association with other diseases e.g. agammaglobulinemia, diabetes  
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Miskott-Aldrich  
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic  
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,  
CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial  
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and  
CC acute intermittent porphyria. The polymorphic forms can also be used in  
CC forensics to identify individuals.

XX  
SQ Sequence 29 BP; 5 A; 7 C; 7 G; 9 T; 1 other;

Query Match 60.0%; Score 18; DB 21; Length 29;

Best Local Similarity 80.8%; Pred. No. 3.4e+02;

Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGACATGATGTAACCC 26

DB 26 ACCATCTGCGCYAACATGATGTAACCC 1

Search completed: June 21, 2003, 22:26:22  
Job time : 165.531 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 ; Search time 35.625 Seconds  
(without alignments)  
258.254 Million cell updates/sec

Title: US-09-964-666-11  
Perfect score: 30  
Sequence: 1 ATCAACCTGCGACATGTGAACCCATC 30

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PTC10S.COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	62.0	47	4	US-09-641-638-659 Sequence 659, App
2	15.2	50.7	20	4	US-09-280-805-259 Sequence 259, App
3	15	50.0	42	4	US-09-171-425-2 Sequence 2, Appl
4	15	50.0	48	4	US-09-171-425-6 Sequence 6, Appl
5	15	50.0	48	4	US-09-171-425-7 Sequence 7, Appl
6	14.8	48.3	26	2	US-08-747-535-17 Sequence 17, Appl
7	14.8	48.3	29	3	US-09-009-913-171 Sequence 171, App
8	14.6	48.7	31	1	US-08-256-368-14 Sequence 14, Appl
9	14.6	48.7	41	4	US-09-297-269-36 Sequence 36, Appl
10	14.4	48.0	30	1	US-07-718-490-2 Sequence 2, Appl
11	14.4	48.0	50	1	US-07-718-490-1 Sequence 1, Appl
12	14.2	47.3	34	1	US-08-471-496-7 Sequence 7, Appl
13	14.2	47.3	34	2	US-08-894-840-7 Sequence 7, Appl
14	14.2	47.3	34	3	US-09-139-675-7 Sequence 7, Appl
15	14	46.7	28	4	US-08-853-774-11 Sequence 11, Appl
16	14	46.7	33	3	US-08-469-318-171 Sequence 171, App
17	14	46.7	33	3	US-08-468-609A-171 Sequence 171, App
18	14	46.7	33	3	US-08-471-045-53 Sequence 53, Appl
19	14	46.7	33	3	US-08-469-712A-53 Sequence 53, Appl
20	14	46.7	33	4	US-08-875-533-26 Sequence 26, Appl
21	14	46.7	33	4	US-08-446-871-53 Sequence 53, Appl
22	14	46.7	33	4	US-08-446-872A-171 Sequence 171, App
23	14	46.7	33	4	US-08-468-910-53 Sequence 53, Appl
24	14	46.7	33	4	US-08-761-907-53 Sequence 53, Appl
25	14	46.7	33	4	US-08-762-227A-171 Sequence 171, App
26	14	46.7	33	5	PCT-US95-01185-171 Sequence 171, App
27	14	46.7	37	4	US-09-344-888A-19 Sequence 19, Appl

C 28	14	46.7	38	1	US-08-642-255-22 Sequence 22, Appl
C 29	14	46.7	38	3	US-08-475-411A-53 Sequence 53, Appl
C 30	14	46.7	38	4	US-08-478-029A-53 Sequence 53, Appl
C 31	13.8	46.0	20	1	US-07-991-199D-14 Sequence 14, Appl
C 32	13.8	46.0	20	4	US-09-593-589-81 Sequence 81, Appl
C 33	13.8	46.0	30	4	US-08-870-511-28 Sequence 28, Appl
C 34	13.8	46.0	43	1	US-08-766-014-10 Sequence 10, Appl
C 35	13.8	46.0	46	4	US-08-707-860D-1 Sequence 1, Appl
C 36	13.6	45.3	21	3	US-09-159-274-22 Sequence 22, Appl
C 37	13.6	45.3	30	1	US-07-789-179-7 Sequence 7, Appl
C 38	13.6	45.3	30	1	US-08-240-712-16 Sequence 16, Appl
C 39	13.6	45.3	30	1	US-08-443-890-16 Sequence 16, Appl
C 40	13.6	45.3	30	1	US-08-444-942-7 Sequence 7, Appl
C 41	13.6	45.3	30	1	US-08-444-105-7 Sequence 7, Appl
C 42	13.6	45.3	30	1	US-08-444-939-7 Sequence 7, Appl
C 43	13.6	45.3	30	2	US-08-444-991-7 Sequence 7, Appl
C 44	13.6	45.3	30	2	US-08-450-733-7 Sequence 7, Appl
C 45	13.6	45.3	30	4	US-09-058-562-16 Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-09-641-638-659  
Sequence 659, Application US/09641638  
Patent No. 6432648  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bouguetelret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
FILE REFERENCE: GENSET.051CPI  
CURRENT FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 659  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 10-520-256 : polymorphic base C or T  
US-09-641-638-659

Query Match  
Best Local Similarity 77.8%; Score 18.6; DB 4; Length 47;  
Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

DB 17 ACCATCTGCGTACACGCGTGAACCC 43

RESULT 2  
US-09-280-805-259  
Sequence 259, Application US/09280805  
Patent No. 6184212  
GENERAL INFORMATION:  
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.  
APPLICANT: Graham, Brett P. Monia

```

: TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MD2
: TITLE OF INVENTION: EXPRESSION
: NUMBER OF SEQUENCES: 271
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Law Offices of Jane Massey Licata
: STREET: 66 East Main Street
: CITY: Marlton
: STATE: NJ
: COUNTRY: U.S.A.
: ZIP: 08053
: COMPUTER READABLE FORM:
: MEDIA TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
: COMPUTER: IBM PC
: OPERATING SYSTEM: WINDOWS 95
: SOFTWARE: WORDPERECT 6.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/280,805
: FILING DATE: herewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/048,810
: FILING DATE: March 26, 1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Licata, Jane Massey
: REGISTRATION NUMBER: 32,257
: REFERENCE/DOCKET NUMBER: ISPH-0346
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 609-810-1515
: TELEFAX: 609-810-1454
: INFORMATION FOR SEQ ID NO: 259:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: ANTI-SENSE: Yes
: US-09-280-805-259

Query Match          50.7%; Score 15.2; DB 4; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      8 TGGCGACATGGTGAACCC 27
        ||||| ||||| ||||| |||||
DB      1 TGGCTAACACGCGTGAACCC 20

RESULT 3
US-09-171-425-2
: Sequence 2, Application US/09171425A
: Patent No. 6465438
: GENERAL INFORMATION:
: APPLICANT: Schorr, Joachim
: APPLICANT: Baker, Henry J.
: APPLICANT: Smith, Bruce F.
: TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
: FILE REFERENCE: 08909/003001
: CURRENT APPLICATION NUMBER: US/09/171,425A
: CURRENT FILING DATE: 1998-10-19
: EARLIER APPLICATION NUMBER: PCT/EP97/01943
: EARLIER FILING DATE: 1996-04-19
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 42
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetically generated oligonucleotides
: US-09-171-425-2

Query Match          50.0%; Score 15; DB 4; Length 42;
Best Local Similarity 78.3%; Pred. No. 7.6e+02;
Matches 78; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 ATCAACCTGGCGACATGCTGAA 23
        ||||| ||||| ||||| |||||
DB      13 ATCAACCTGGCTAGAGAGAA 35
```

```

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 ATCAACCTGGCGACATGCTGAA 23
        ||||| ||||| ||||| |||||
DB      13 ATCAACCTGGCTAGAGAGAA 35

RESULT 4
US-09-171-425-6
: Sequence 6, Application US/09171425A
: Patent No. 6465438
: GENERAL INFORMATION:
: APPLICANT: Schorr, Joachim
: APPLICANT: Baker, Henry J.
: APPLICANT: Smith, Bruce F.
: TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
: FILE REFERENCE: 08909/003001
: CURRENT APPLICATION NUMBER: US/09/171,425A
: CURRENT FILING DATE: 1998-10-19
: EARLIER APPLICATION NUMBER: PCT/EP97/01943
: EARLIER FILING DATE: 1996-04-19
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 48
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetically generated oligonucleotides
: US-09-171-425-6

Query Match          50.0%; Score 15; DB 4; Length 48;
Best Local Similarity 78.3%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 ATCAACCTGGCGACATGCTGAA 23
        ||||| ||||| ||||| |||||
DB      19 ATCAACCTGGCTAGAGAGAA 41

RESULT 5
US-09-171-425-7/c
: Sequence 7, Application US/09171425A
: Patent No. 6465438
: GENERAL INFORMATION:
: APPLICANT: Schorr, Joachim
: APPLICANT: Baker, Henry J.
: APPLICANT: Smith, Bruce F.
: TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
: FILE REFERENCE: 08909/003001
: CURRENT APPLICATION NUMBER: US/09/171,425A
: CURRENT FILING DATE: 1998-10-19
: EARLIER APPLICATION NUMBER: PCT/EP97/01943
: EARLIER FILING DATE: 1996-04-19
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7
: LENGTH: 48
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetically generated oligonucleotides
: US-09-171-425-7

Query Match          50.0%; Score 15; DB 4; Length 48;
Best Local Similarity 78.3%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 ATCAACCTGGCGACATGCTGAA 23
        ||||| ||||| ||||| |||||
DB      34 ATCAACCTGGCTAGAGAGAA 12
```

```

RESULT 6
US-08-747-536-17
; Sequence 17, Application US/08747536
; Patent No. 5968737
; GENERAL INFORMATION:
; APPLICANT: Ali-Osman, Francis
; APPLICANT: Lopez-Berestein, Gabriel
; APPLICANT: Buolamwini, John
; APPLICANT: Antoun, Gamil
; APPLICANT: Lo, Hui-Wen
; APPLICANT: Keller, Charles
; APPLICANT: Akande, Olanike
; TITLE OF INVENTION: GLUTATHIONE S-TRANSFERASE (GST) GENES IN
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,536
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-747-536-17

Query Match          49.3%; Score 14.8; DB 2; Length 26;
Best Local Similarity 88.9%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      6 CCTGGCAACATGCTGAA 23
       ||||| | |||||
Db      5 CCTGGTGCACATGCTGAA 22

RESULT 7
US-09-009-913-171
; Sequence 171, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axy's Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ashtma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

```

```

; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-009-913-171

Query Match          49.3%; Score 14.8; DB 3; Length 29;
Best Local Similarity 88.9%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      6 CCTGGCAACATGCTGAA 23
       ||||| | |||||
Db      9 CCTGGCTAACACGCTGAA 26

RESULT 8
US-08-256-368-14/c
; Sequence 14, Application US/08256368
; Patent No. 5641649
; GENERAL INFORMATION:
; APPLICANT: Stanchi, Ombretta
; APPLICANT: Negro, Alessandro
; APPLICANT: Callegaro, Lanfranco
; TITLE OF INVENTION: Expression Of Osteogenic Factor Op-1
; TITLE OF INVENTION: In Cells Of Spodoptera Frugiperda Infected With
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,368
; FILING DATE: 22-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 259-243P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)205-8000
; TELEFAX: (703)205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs

```

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "PCR primer"  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US:08-256-368-14

Query Match 48.7%; Score 14.6; DB 1; Length 31;  
Best Local Similarity 69.0%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 2 TCACCTGGCGAATGTCGACCCCATC 30  
||||| ||| ||| ||| ||| ||| |||  
Db 30 TCACCTGGCGAATGTCGACCTGCAC 2

RESULT 9  
US-09-297-269-36  
Sequence 36, Application US/09297269  
Patent No. 6451557  
GENERAL INFORMATION:  
APPLICANT: VAUGHAN, Paul R.  
APPLICANT: GALANTIS, Maria  
APPLICANT: RAMSHAW, John A.M.  
APPLICANT: WERKMEISTER, Jerome A.  
TITLE OF INVENTION: A METHOD FOR PRODUCING, IN YEAST, A HYDROXYLATED TRIPLE  
TITLE OF INVENTION: HELICAL PROTEIN, AND YEAST HOST CELLS USEFUL IN SAID  
FILE OF INVENTION: METHOD (As Amended)  
FILE REFERENCE: 054094  
CURRENT APPLICATION NUMBER: US/09/297,269  
EARLIER FILING DATE: 1999-04-28  
EARLIER APPLICATION NUMBER: P03310  
EARLIER FILING DATE: 1996-10-29  
EARLIER APPLICATION NUMBER: P04306  
EARLIER FILING DATE: 1996-12-19  
EARLIER APPLICATION NUMBER: PCT/US97/00721  
EARLIER FILING DATE: 1997-10-29  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 41  
TYPE: DNA  
ORGANISM: synthetic construct  
US-09-297-269-36

Query Match 48.7%; Score 14.6; DB 4; Length 41;  
Best Local Similarity 81.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 ACCTGGCGAATGTCGAC 25  
||||| ||| ||| ||| ||| |||  
Db 14 ACCTGGCGAATGTCGAC 34

RESULT 10  
US-07-718-490-2/c  
Sequence 2, Application US/07718490  
Patent No. 5340716  
GENERAL INFORMATION:  
APPLICANT: Ullman, Edwin F.  
APPLICANT: Kirakossian, Hrair  
APPLICANT: Pease, John S.  
APPLICANT: Danilooff, Yuri  
APPLICANT: Wagner, Daniel B.  
TITLE OF INVENTION: Assay Method Utilizing Photoactivated  
TITLE OF INVENTION: Chemiluminescent Label  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syntex (U.S.A.) Inc.  
STREET: 3401 Hillview Avenue  
CITY: Palo Alto

STATE: California  
COUNTRY: U.S.A.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/718,490  
FILING DATE: 19910620  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Letterer, Theodore J.  
REGISTRATION NUMBER: 28,319  
REFERENCE/DOCKET NUMBER: 27340/ DO-1557  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 852-1091  
TELEFAX: (415) 496-3529  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
ORIGINAL SOURCE:  
ORGANISM: Escherichia coli  
STRAIN: K12 DNAJ  
INDIVIDUAL ISOLATE: Synthetic  
US-07-718-490-2

Query Match 48.0%; Score 14.4; DB 1; Length 30;  
Best Local Similarity 75.0%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 TCACCTGGCGAATGTCGAC 25  
||||| ||| ||| ||| ||| |||  
Db 29 TCACCTGGCGAATGTCGAC 6

RESULT 11  
US-07-718-490-1  
Sequence 1, Application US/07718490  
Patent No. 5340716  
GENERAL INFORMATION:  
APPLICANT: Ullman, Edwin F.  
APPLICANT: Kirakossian, Hrair  
APPLICANT: Pease, John S.  
APPLICANT: Danilooff, Yuri  
APPLICANT: Wagner, Daniel B.  
TITLE OF INVENTION: Assay Method Utilizing Photoactivated  
TITLE OF INVENTION: Chemiluminescent Label  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syntex (U.S.A.) Inc.  
STREET: 3401 Hillview Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/718,490  
FILING DATE: 19910620  
CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:  
 NAME: Leitner, Theodore J.  
 REGISTRATION NUMBER: 28,319  
 REFERENCE/DOCKET NUMBER: 27340/ DO-1557  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 852-1091  
 TELEFAX: (415) 496-3529  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 50 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)T  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: Internal  
 ORIGINAL SOURCE:  
 ORGANISM: Escherichia coli  
 STRAIN: K12 DNAJ  
 INDIVIDUAL ISOLATE: Synthetic  
 US-07-718-490-1

Query Match 48.0%; Score 14.4; DB 1; Length 50;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;  
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 TCACCTGGCGAATGTCGAC 25  
 Db 12 TGAAGCGGCGACATGCGCCAC 35

RESULT 12  
 US-08-471-496-7  
 Sequence 7, Application US/08471496  
 Patent No. 5798223  
 GENERAL INFORMATION:  
 APPLICANT: LI, YI  
 APPLICANT: CAO, LIANG  
 APPLICANT: ROSEN, CRAIG  
 TITLE OF INVENTION: HUMAN AMINE TRANSPORTER  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVENUE, SUITE 600  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,496  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/US95/02645  
 FILING DATE: 01-MAR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.0830001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2540  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 34 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

MOLECULE TYPE: CDNA  
 US-08-471-496-7

Query Match 47.3%; Score 14.2; DB 1; Length 34;  
 Best Local Similarity 70.4%; Pred. No. 1.6e+03;  
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 CAACCTGGCGAATGTCGACCCAT 29  
 Db 4 CAAGCTTGCACCATCTGCGGCCAT 30

RESULT 13  
 US-08-894-840-7  
 Sequence 7, Application US/08894840  
 Patent No. 5859200  
 GENERAL INFORMATION:  
 APPLICANT: LI, YI  
 APPLICANT: CAO, LIANG  
 APPLICANT: ROSEN, CRAIG A.  
 TITLE OF INVENTION: HUMAN AMINE TRANSPORTER  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVENUE, SUITE 600  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3934  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/894,840  
 FILING DATE: 29-AUG-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.0830000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 371-2540  
 TELEFAX: (202) 371-2540  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 34 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-08-894-840-7

Query Match 47.3%; Score 14.2; DB 2; Length 34;  
 Best Local Similarity 70.4%; Pred. No. 1.6e+03;  
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 CAACCTGGCGAATGTCGACCCAT 29  
 Db 4 CAAGCTTGCACCATCTGCGGCCAT 30

RESULT 14  
 US-09-139-675-7  
 Sequence 7, Application US/09139675A  
 Patent No. 6117426  
 GENERAL INFORMATION:  
 APPLICANT: LI, YI  
 APPLICANT: CAO, LIANG  
 APPLICANT: ROSEN, CRAIG  
 TITLE OF INVENTION: Human Amine Transporter  
 FILE REFERENCE: 1488.0830003  
 CURRENT APPLICATION NUMBER: US/09/139,675A

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: CURRENT FILING DATE: 1998-08-25
: EARLIER APPLICATION NUMBER: WO PCT/US95/02645
: EARLIER FILING DATE: 1995-03-01
: EARLIER APPLICATION NUMBER: US 08/471,486
: EARLIER FILING DATE: 1995-06-06
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO: 7
: LENGTH: 34
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-139-675-7

```

```

Query Match          47.3%: Score 14.2; DB 3: Length 34;
Best Local Similarity 70.4%: Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      3 CAACCTGGCGAAGGTGTAACCCCAT 29
      111111111111111111111111
Db      4 CAAGCTGGCCACCATGCTGCGCCCAT 30

```

```

RESULT 15
US-08-853-774-11
: Sequence 11, Application US/08853774
: Patent No. 6265557
: GENERAL INFORMATION:
: APPLICANT: Diamond, David
: APPLICANT: Nehlsen-Cannarella, Sandra
: APPLICANT: Fagoaga, Omar
: APPLICANT: Szalay, Aladar
: TITLE OF INVENTION: ABO HISTO-BLOOD GROUP O ALLELES OF THE BABOON
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Knobb, Martens, Olson & Bear
: STREET: 620 Newport Center Drive Sixteenth Flo
: CITY: Newport Beach
: STATE: CA
: COUNTRY: USA
: ZIP: 92660
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/853,774
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Altman, Daniel E.
: REGISTRATION NUMBER: 34,115
: REFERENCE/DOCKET NUMBER: LOMAIMM.100A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 714/760-0404
: TELEFAX: 714/760-9503
: TELEX:
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-853-774-11

```

```

Query Match          46.7%: Score 14; DB 4: Length 28;
Best Local Similarity 77.3%: Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 8 TGGCGAACAATGCTGAACCCCAT 29

```

Db      5 TGGCAACACAGTTAACCACAT 26

```

Search completed: June 22, 2003, 00:01:32  
Job time : 36.625 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 22:26:37 ; Search time 88.5938 Seconds  
(without alignments)  
496.907 Million cell updates/sec

Title: US-09-964-666-11

Perfect score: 30  
Sequence: 1 ATCAACCTGGCGACATGCTGAACCCCATC 30

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published.Applications\_NA.\*  
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3: /cgn2\_6/ptodata/2/pubpna/US06\_PUB\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
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14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	30	100.0	30	10	US-09-964-666-11
3	30	100.0	30	10	US-09-964-412-11
4	19	63.3	49	9	US-09-860-670-233
5	16.8	56.0	30	9	US-10-085-906-77
6	16.6	55.3	29	9	US-09-530-139-69
7	16.2	54.0	22	9	US-09-530-139-70
8	16.2	54.0	24	10	US-09-885-441-35
9	16	53.3	32	9	US-10-123-170-17
10	15.2	50.7	20	10	US-09-752-983-259
11	15.2	50.7	20	10	US-09-800-631-32
12	15.2	50.7	31	10	US-09-801-274-1110
13	15.2	50.7	36	9	US-09-877-478-6391
14	15.2	50.7	37	9	US-09-877-478-4044
15	15	50.0	25	9	US-10-098-2638-8701
16	15	50.0	41	9	US-10-239-804-23
17	15	50.0	41	9	US-10-239-804-36
18	14.8	49.3	20	9	US-09-771-933-148
19	14.6	48.7	26	10	US-09-740-668A-55

20	14.6	48.7	30	9	US-10-085-906-241	Sequence 241, App
21	14.4	48.0	37	10	US-09-755-665-108	Sequence 108, App
22	14.2	47.3	30	10	US-09-964-277-15	Sequence 15, App
23	14.2	47.3	31	9	US-09-924-125-4	Sequence 4, App
24	14.2	47.3	34	10	US-09-987-025-12	Sequence 12, App
25	14.2	47.3	37	9	US-09-780-533A-4302	Sequence 4302, App
26	14.2	47.3	37	9	US-09-780-533A-4387	Sequence 4387, App
27	14.2	47.3	37	9	US-09-877-478-4122	Sequence 4122, App
28	14.2	47.3	37	9	US-09-930-423-2915	Sequence 2915, App
29	14	46.7	24	9	US-09-940-185-2688	Sequence 2688, App
30	14	46.7	25	9	US-10-098-2638-25783	Sequence 25783, App
31	14	46.7	30	9	US-09-832-292-24	Sequence 24, App
32	13.8	46.0	20	9	US-10-025-201-13	Sequence 13, App
33	13.8	46.0	25	9	US-10-192-926-18	Sequence 18, App
34	13.8	46.0	37	9	US-09-930-423-2785	Sequence 2785, App
35	13.8	46.0	37	9	US-09-930-423-2860	Sequence 2860, App
36	13.8	46.0	46	9	US-10-146-938-1	Sequence 1, App
37	13.6	45.3	20	9	US-10-085-906-365	Sequence 365, App
38	13.6	45.3	23	10	US-09-529-063-86	Sequence 86, App
39	13.6	45.3	30	9	US-10-085-906-44	Sequence 44, App
40	13.6	45.3	30	9	US-09-864-636A-1614	Sequence 1614, App
41	13.6	45.3	31	10	US-09-801-274-1365	Sequence 1365, App
42	13.6	45.3	33	9	US-10-155-233-10	Sequence 10, App
43	13.6	45.3	37	9	US-09-730-289B-2710	Sequence 2710, App
44	13.6	45.3	37	9	US-09-780-533A-4376	Sequence 4376, App
45	13.6	45.3	37	9	US-09-877-478-4115	Sequence 4115, App

#### ALIGNMENTS

RESULT 1  
US-09-964-667-11  
Sequence 11, Application US/09964667  
Publication No. US20030033621A1  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
Wands, Jack R.  
TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS: Stern, Kessler, Goldstein & Fox, P.L.L.C.  
ADDRESS: 1100 New York Ave., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/09/964,667  
FILING DATE: 28-Sep-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0609,4370000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-964-667-11

Query Match 100.0%; Score 30; DB 9; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACAATGTTGAACCCCATC 30  
1 ATCAACCTGGCGAACAATGTTGAACCCCATC 30

RESULT 2

US-09-964-666-11  
Sequence 11, Application US/09964666  
Patent No. US20020104108A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-964-666-11

Query Match 100.0%; Score 30; DB 10; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACAATGTTGAACCCCATC 30  
1 ATCAACCTGGCGAACAATGTTGAACCCCATC 30

RESULT 3

US-09-964-412-11  
Sequence 11, Application US/09964412  
Patent No. US20020129391A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-964-412-11

Query Match 100.0%; Score 30; DB 10; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.00063;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACAATGTTGAACCCCATC 30  
1 ATCAACCTGGCGAACAATGTTGAACCCCATC 30

RESULT 4

US-09-860-670-233  
Sequence 233, Application US/09860670  
Patent No. US20020165137A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA127P1

CURRENT APPLICATION NUMBER: US/09/860,670

CURRENT FILING DATE: 2001-05-21

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 289

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 233

LENGTH: 49

TYPE: DNA

ORGANISM: Homo sapiens

US-09-860-670-233

Query Match 63.3%; Score 19; DB 9; Length 49;  
Best Local Similarity 81.5%; Pred. No. 43;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACAATGTTGAACCCCATC 27  
1 ATCAACCTGGCGAACAATGTTGAACCCCATC 27

RESULT 5

```
US-10-085-906-77/c
; Sequence 77, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-77
```

```
Query Match          56.0%: Score 16.8; DB 9; Length 30;
Best Local Similarity 90.0%: Pred. No. 3.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      8 TGGCGAACAATGTTGAACCC 27
          ||||| ||||| ||||| |||
Db       30 TGGCCAAACATGTGTAACCC 11
```

```
RESULT 6
US-09-530-139-69/c
; Sequence 69, Application US/09530139
; Publication No. US20030092892A1
; GENERAL INFORMATION:
; APPLICANT: FREMKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDERBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOGT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-530-139-69
```

```
Query Match          55.3%: Score 16.6; DB 9; Length 29;
Best Local Similarity 82.6%: Pred. No. 4.5e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      5 ACCTGGCAACAATGTTGAACCC 27
          ||||| ||||| ||| ||||| |
Db       26 ACCTGGTGAACCTGTGAACAC 4
```

```
RESULT 7
US-09-530-139-70
```

```
; Sequence 70, Application US/09530139
; Publication No. US20030092892A1
; GENERAL INFORMATION:
; APPLICANT: FREMKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDERBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOGT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-530-139-70
```

```
Query Match          54.0%: Score 16.2; DB 9; Length 22;
Best Local Similarity 85.7%: Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      5 ACCTGGCAACAATGTTGAACC 25
          ||||| ||||| ||| ||||| |
Db       1 ACCTGGTGAACCTGTGAACCC 21
```

```
RESULT 8
US-09-885-441-35/c
; Sequence 35, Application US/09885441
; Patent No. US20020146407A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human Eosinophil Serine
; FILE REFERENCE: 04974.00512
; CURRENT APPLICATION NUMBER: US/09/885,441
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/212,844
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/244,171
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: US 60/279,766
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-885-441-35
```

```
Query Match          54.0%: Score 16.2; DB 10; Length 24;
Best Local Similarity 85.7%: Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      7 CTGGCGAACAATGTTGAACCC 27
          ||||| ||||| ||||| ||||| ||
Db       24 CTGGTGAACAATGTTGAACCC 4
```

```
RESULT 9
US-10-123-170-17
; Sequence 17, Application US/10123170
```

Publication No. US20030008277A1  
GENERAL INFORMATION:  
APPLICANT: ESCRIOU, NICOLAS  
APPLICANT: VAN DER WERF, SYLVIE  
APPLICANT: VIEIRA-MACHADO, ALEXANDRE  
APPLICANT: MAFANH, NADIA  
TITLE OF INVENTION: RECOMBINANT SEGMENTED NEGATIVE STRAND VIRUS CONTAINING BICISTRONIC  
TITLE OF INVENTION: SEGMENT WITH A DUPLICATION OF ITS 3' NONCODING FLANKING SEQUENCE  
TITLE OF INVENTION: AND THERAPEUTIC COMPOSITIONS CONTAINING THE SAME  
FILE REFERENCE: 221283US0  
CURRENT APPLICATION NUMBER: US/10/123,170  
CURRENT FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: 60/283,957  
PRIOR FILING DATE: 2001-04-17  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 17  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic DNA  
US:10-123-170-17

Query Match 53.3%; Score 16; DB 9; Length 32;  
Best Local Similarity 79.2%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 ACCTGGGACATGCTGTAACCCCA 28  
DB 2 ACCTCGAGACATGAGAGACATCA 25

## RESULT 10

US-09-752-983-259

Sequence 259, Application US/09/752983

Patent No. US20010016575A1

GENERAL INFORMATION:

APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.

APPLICANT: Graham, Brett P. Monia

TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2

NUMBER OF SEQUENCES: 271

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Jane Massey Licata

STREET: 66 East Main Street

CITY: Marlton

STATE: NJ

COUNTRY: U.S.A.

ZIP: 08053

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PC

OPERATING SYSTEM: WINDOWS 95

SOFTWARE: WORDPERFECT 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/752,983

FILING DATE: 02-Jan-2001

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/280,805

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Licata, Jane Massey

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0346

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-810-1515

TELEFAX: 609-810-1454

INFORMATION FOR SEQ ID NO: 259:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

Type: Nucleic Acid

STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-09-752-983-259

Query Match 50.7%; Score 15.2; DB 10; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 8 TGGCGAACATGCTGTAACCC 27  
DB 1 TGGCTAACACGGTGAACCC 20

## RESULT 11

US-09-800-631-32/c

Sequence 32, Application US/09800631

Patent No. US2002008228A1

GENERAL INFORMATION:

APPLICANT: Hong Zhang

APPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST E

FILE REFERENCE: ISPH-0544

CURRENT APPLICATION NUMBER: US/09/800,631

CURRENT FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: US/09/657,346

PRIOR FILING DATE: 2000-09-07

NUMBER OF SEQ ID NOS: 175

SEQ ID NO 32

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-800-631-32

Query Match 50.7%; Score 15.2; DB 10; Length 20;  
Best Local Similarity 85.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 CTGCGAACATGCTGTAACCC 26  
DB 20 CTGACCAACATGCTGAACCC 1

RESULT 12

US-09-801-274-1110/c

Sequence 1110, Application US/09801274

Patent No. US20020032319A1

GENERAL INFORMATION:

APPLICANT: Cargill, Michele

APPLICANT: Ireland, James S.

TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS

FILE REFERENCE: 2825.2009-001

CURRENT APPLICATION NUMBER: US/09/801,274

CURRENT FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: US 60/187,510

PRIOR FILING DATE: 2000-03-07

PRIOR APPLICATION NUMBER: US 60/206,129

PRIOR FILING DATE: 2000-05-22

NUMBER OF SEQ ID NOS: 1802

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1110

LENGTH: 31

TYPE: DNA

ORGANISM: Homo sapiens

US-09-801-274-1110

Query Match 50.7%; Score 15.2; DB 10; Length 31;  
Best Local Similarity 77.3%; Pred. No. 1.8e+03;  
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;



Mon Jun 23 10:01:49 2003

us-09-964-666-11.Length\_Limit\_\_50.rnpb

Page 6

Db                   |||||   |   |||||   |||   |||  
2 TCAACSTCGGAGACACGTCAC 24

Search completed: June 22, 2003, 03:18:19  
Job time : 91.5938 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:28:37 ; Search time 1295.86 Seconds  
(without alignments)  
374.936 Million cell updates/sec

Title: US-09-964-666-11

Perfect score: 30  
Sequence: 1 ATCAACCTGCGACATGCTGACCCCATC 30

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estopl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_estc3:\*  
13: gb\_estc4:\*  
14: gb\_estl5:\*  
15: em\_estfun:\*  
16: em\_estrom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pin:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21.6	72.0	50	9	AU105733
C 2	21.2	70.7	50	9	AU106806
C 3	20.8	69.3	33	14	N80349
C 4	20.6	68.7	50	9	AU102526
C 5	20.6	68.7	50	9	AU105702
C 6	20.4	68.0	44	9	AA492220

Result No.	Score	Query Match	Length	DB ID	Description
C 7	20.2	67.3	50	9	AU103189
C 8	19	63.3	33	14	T53436
C 9	19	63.3	50	9	AU102524
C 10	19	63.3	50	9	AU102525
C 11	19	63.3	50	9	AU102528
C 12	19	63.3	50	9	AU102530
C 13	19	63.3	50	9	AU102535
C 14	19	63.3	50	9	AU102667
C 15	19	63.3	50	9	AU103194
C 16	19	63.3	50	9	AU104029
C 17	19	63.3	50	9	AU105991
C 18	19	63.3	50	9	AU106616
C 19	18.2	60.7	37	14	H56911
C 20	18	60.0	50	9	AU105734
C 21	17.8	59.3	48	9	AU258691
C 22	17.6	58.7	47	14	H99103
C 23	17.6	58.7	50	9	AU102536
C 24	17.6	58.7	50	9	AU104439
C 25	17.4	58.0	50	9	AU102521
C 26	17.4	58.0	50	9	AU102528
C 27	17.4	58.0	50	9	AU103192
C 28	17.4	58.0	50	9	AU105233
C 29	17.2	57.3	48	9	AA973269
C 30	16.6	55.3	50	9	AU103183
C 31	16.6	55.3	50	9	AU105742
C 32	16.4	54.7	36	14	R91494
C 33	16.4	54.7	46	9	AA912807
C 34	15.8	52.7	50	9	AU102522
C 35	15.8	52.7	50	9	AU102531
C 36	15.8	52.7	50	9	AU104028
C 37	15.8	52.0	50	9	AU104437
C 38	15.6	52.0	32	17	AZ309847
C 39	15.2	50.7	40	14	H82905
C 40	15	50.0	47	14	H88764
C 41	14.8	49.3	47	14	C20880
C 42	14.8	49.3	50	9	AU1024893
C 43	14.6	48.7	50	9	AU244156
C 44	14.6	48.7	48	14	N57213
C 45	14.4	48.0	32	14	R05734

## ALIGNMENTS

RESULT 1  
LOCUS AU105733/c 50 bp mRNA linear EST 30-AUG-2001  
DEFINITION AU105733 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
ACCESSION COL01940, mRNA sequence.  
VERSION AU105733  
KEYWORDS AU105733.1 GI:13555254  
SOURCE EST.  
ORGANISM human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata  
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
JOURNAL MEDLINE  
COMMENT 21270072  
Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: ysuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
,S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers

	source	1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="COI01940" /clone_lib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylflumate treated U937 cells"
BASE COUNT	7 a 7 c 15 g 21 t	
ORIGIN		
Query Match	72.0%;	Score 21.6; DB 9; Length 50;
Best Local Similarity	85.7%;	Fred. No. 75;
Matches	24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Oy	1 ATCAACCTGGCAGCATGTGTAACCCA 28                               46 ACACACCTGGCCACATGTGTGAACCCA 19	
Db		
RESULT 2		
AU106806/c	50 bp mRNA linear EST 30-AUG-2001	
LOCUS	AU106806 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone	
DEFINITION	LNC05691, mRNA sequence.	
ACCESSION	AU106806	
VERSION	AU106806.1 GI:13556327	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 50) Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hatake, H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki, Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)	
TITLE	21270072	
JOURNAL	Contact: Yutaka Suzuki	
MEDLINE	Department of Virology	
COMMENT	Institute of Medical Science, University of Tokyo 4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers 1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="LNC05691" /clone_lib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylflumate treated U937 cells"	
BASE COUNT	14 a 10 c 12 g 14 t	
ORIGIN		
Query Match	70.7%;	Score 21.2; DB 9; Length 50;
Best Local Similarity	88.5%;	Fred. NO. 1.1e+02;
Matches	23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
Oy	1 ATCAACCTGGCAGCATGTGTAACCC 26                               42 ATCAACCTGGTCACACATGTGTAAACC 17	
Db		
RESULT 3		
N80349	33 bp mRNA linear EST 02-APR-1996	
LOCUS	zai3c12.r1 Soares fetal liver spleen INTLS Homo sapiens cDNA clone	
DEFINITION	IMAGE:292438.5' similar to gb U13704 HUMSCALUB Human scRNA molecule , transcribed from Alu (rRNA); gp:X53795_rnal INDUCIBLE MEMBRANE	

[illegible]



TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE	21270072
COMMENT	Contact: Yutaka Suzuki

**FEATURES**

Location/Qualifiers

Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yuzuzuki@ims.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo Nakagawa, K., Maruyama, A., Suyama, A. and Sugano, S.  
Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COLF141"
/clone_1b="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated 0937 cells"
9 a 9 c 17 g 15 t

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Query Match	68.7%	Score 20.6	DB 9	Length 50
Best Local Similarity	85.2%	Pred. No. 1.9e+02		
Matches 23	Conservative 0	Mismatches 4	Indels 0	Gaps 0

QY	1	ATCAACCTGGCGACATGGTGAACCCC	27
Db	43	ACCAAGCCTGGCCACATGGTGAACCC	17

RESULT 5	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS
AU105702	AU105702	50 bp mRNA	AU105702	AU105702	linear EST 30-Aug-2001
		Sugano Homo sapiens cDNA library			Homo sapiens cDNA clone
		HR011393, mRNA sequence.			
		AU105702			
		AU105702.1 GI:1355223			
		EST.			

ORGANISM	Homosapiens	Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100

CAGARU, T., IIDA, H., ISHINOBU, T., MIYASHIMA, SUGANO, J., SASE, U., HATAI, H., Ota, T., ISOGAI, T., TANAKA, T., MORISHITA, S., OKUBO, R., SAKAI, Y., NAKAMURA, Y., SUYAMA, A. and SUGANO, S.  
 Diverse transcriptional initiation revealed by fine large-scale

JOURNAL  
MEDLINE  
COMMENT

EMBO Rep. 2 (5), 388-393 (2001)  
21270072  
Contact: Yutaka Suzuki

**FEATURES**  
source  
1. .50  
Location/Qualifiers  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Suganoc,  
S. Construction and characterization of a full length-enriched and  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yuzuki@ims.u-tokyo.ac.jp

BASE COUNT  
ORIGIN

Query Match	68.7%;	Score 20.6;	DB 9;	Length 50;
Best Local Similarity	85.2%;	Pred. No. 1.9e+02;		

Matches	23; Conservative	0; Mismatches	4; Indels	0; Gaps
QY	1 ATCAACCTGGCGAACAATGTTGAACCCC	27	.	
Db	14 ACCAGCCTGGCCACAACATGTTGAACCCC	40	.	

LOCUS	DEFINITION	EST 19-AUG-1997
AA492220	44 bp mRNA linear	
09799404.s1	NCI-CGAP-Pt6 Homo sapiens cDNA clone IMAGE:940974	
	similar to gb:M91159 !!! ALU CLASS E WARNING ENTRY !!! (HUMAN);	
	mRNA sequence.	

ACCESSION	AA492220	GI:2221782
VERSION	AA492220.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS  
1 (bases 1 to 44)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute. Cancer Data Element Dictionary (CDD) 1999. Bethesda, MD: National Cancer Institute; 1999.

Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
COMMENT

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuagui,  
M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.lnl.gov/bdrrp/image/image.html](http://www.bio.lnl.gov/bdrrp/image/image.html)  
Insert Length: 575 Std Error: 0.00  
Seq primer: ~40ml3 fwd, 5' from Amersham  
High quality sequence stop: 1.

FEATURES	Location/Qualifiers
source	1. .44

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:940974"
/clone_lib="NCI-CGAP_Pr6"

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/sex="male"
/tissue_type="prostate"
/lab_host="DH10B"
/ncote="vector: pAMPl0: mRNA made from prostatic
intraepithelial neoplasia (low-grade), cDNA made by
oligo-dt priming. Non-directionally cloned.
size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."

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BASE COUNT	15 a	14 c	7 g	8
ORIGIN				

Query Match	68.0%;	Score 20.4;	DB 9;	Length 44;
Best Local Similarity	80.0%;	Pred. No. 2, 2e+02;		
Matches 24;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;

Db 3 ACCAGCCTGGCCACATGTGTCATACCCACC 32

DEFINITION	Accession	Length	Score	Evalue
AUI03189 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC04023, mRNA sequence.	U03189	28 bp	1.14e+01	2.0e-01

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VERSION      AU103189.1  GI:13552710
KEYWORDS     EST.

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ORGANISM	Human.
SOURCE	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 50)
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hatake,H., Ota,T., Isozaki,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL MEDLINE	EMBO Rep. 2 (5), 388-393 (2001)
COMMENT	21270072 Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES	Location/Qualifiers
SOURCE	1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="HRC04023" /clone_lib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylflunare treated 1937 cells" 6 9 a 7 c 15 g 19 t
BASE COUNT	
ORIGIN	
Query Match	67.3%; Score 20.2; DB 9; Length 50;
Best Local Similarity	88.0%; Pred. No.2.7e+02;
Matches	22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	3 CAACTGGCGAACAATGATGTAACCCC 27 
DB	49 CAGCTGGCAACAATGATGTAACCC 25
RESULT 8	
T53436	T53436 33 bp mRNA linear EST 06-FEB-1995
LOCUS	YAB99a10.s1 Stratiagene placenta (937225) Homo sapiens cDNA clone IMAGE:68826 3' similar to similar to gb:U87338 ACTIVATOR 1 40 KD
DEFINITION	SUBUNIT (HUMAN), mRNA sequence.
ACCESSION	T53436
VERSION	T53436.1 GI:655296
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 33)
AUTHORS	Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisose,S., Dietrich,N., Dubugue,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevisan,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL MEDLINE	Genome Res. 6 (9), 807-828 (1996)
COMMENT	97044478 Other_ESTs: yab99a10.r1 Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence starts: 1 High quality sequence stops: 1 Source: IMAGE Consortium, LNC

This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.  
Trace considered overall poor quality  
Seq primer: -21mJ3  
High quality sequence stop: 1.

FEATURES  
SOURCE location/Qualifiers  
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    /organism="Homo sapiens"  
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    /db\_xref=taxon:9606  
    /clone\_image=68826  
    /clone\_lib="Stratagene placenta (#937225)"  
    /sex="male"  
    /lab\_host="SOER cells (kanamycin resistant)"  
    /note="Organ: Placenta; Vector: pluscript SK-; Site:1:  
Ecobi; Site\_2: XhoI; Cloned unidirectionally. Primer:  
Oligo dT. Caucasian. Average insert size: 1.2 kb; UniZAP  
XR vector: -5' adaptor sequence: 5' GAATTCGGCAGACG 3' -3'  
adaptor sequence: 5' CTCGACTTTTTTTTTTTTTT 3'"

BASE COUNT                 10 a          12 c          7 g          4 t  
ORIGIN

Query Match                                 63.3%; Score 19; DB 14; Length 33;  
Best Local Similarity                 81.5%; Pred. No. 7.3e+02;  
Matches                 22; Conservative     0; Mismatches     5; Indels     0; Gaps     0;

OY     1 ATCAACCTGTGCACAACATCGTAGACC CC 27  
      | | ||||| ||||||| |||||  
Db     7 ACCAGCCGTGCCAACACATCGGAGACCCC 33

RESULT 9  
AIU02524/c                                 50 bp mRNA linear EST 30-AUG-2001

LOCUS AIU02524 Sugano Homo sapiens cdna library Homo sapiens CDNA clone  
DEFINITION COL07268, mRNA sequence.  
VERSION AIU02524  
KEYWORDS AIU02524.1 GI:13552044  
EST.

SOURCE  
human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 50)  
SUZUKI,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,  
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,  
Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL MEDLINE 21270072  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan  
Email: yusuzuki@cims.u-tokyo.ac.jp  
SUZUKI,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,  
S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
SOURCE Location/Qualifiers  
1..50  
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    /clone\_lib="Sugano Homo sapiens CDNA library"  
    /note="Differential display comparison of untreated and  
dimethylmitarlate treated U937 cells"

BASE COUNT                 10 a          12 c          12 g          16 t  
ORIGIN

Query Match                                 63.3%; Score 19; DB 9; Length 50;  
Best Local Similarity                 81.5%; Pred. No. 8.3e+02;  
Matches                 22; Conservative     0; Mismatches     5; Indels     0; Gaps     0;

Qy	1	ATCAACCTGGCGACATGTCGTAACCC	27
	1		
Db	39	ACCAAGCTGGCAACATGTCGTAACCTC	13
RESULT 10			
AU102525/c			
LOCUS	AU102525		
DEFINITION	AU102525 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone		
ACCESSION	COL08447		
VERSION	AU102525		
KEYWORDS	AU102525.1 GI:13552045		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 50)		
	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata		
	,H., Ota,T., Isegaai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki		
	,Y., Nakamura,Y., Suyama,A. and Sugano,S.		
	Diverse transcriptional Initiation revealed by fine, large-scale		
	mapping of mRNA start sites		
	EMBO Rep. 2 (5), 388-393 (2001)		
	21270072		
JOURNAL	Contact: Yutaka Suzuki		
MEDLINE	Institute of Medical Science, University of Tokyo		
COMMENT	Department of Medical Science, University of Tokyo		
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan		
	Email: yusuzuki@ims.u-tokyo.ac.jp		
	Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano		
	,S. Construction and characterization of a full length-enriched and		
	a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).		
FEATURES	Location/Qualifiers		
Source	1..50		
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	/note="Differential display comparison of untreated and		
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ORIGIN			
Query Match	63.3%	Score 19:	DB 9: Length 50:
Best Local Similarity	81.5%	Pred. NO. 8.3e+02:	
Matches	22:	Conservative 0:	Mismatches 5: Indels 0: Gaps 0:
Qy	1	ATCAACCTGGCGACATGTCGTAACCC	27
	1		
Db	41	ACCAAGCTGGCAACATGTCGTAACAC	15
RESULT 11			
AU102525/c			
LOCUS	AU102525		
DEFINITION	AU102525 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone		
ACCESSION	HR007143		
VERSION	AU102529		
KEYWORDS	AU102529.1 GI:13552049		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 50)		
	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata		
	,H., Ota,T., Isegaai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki		
	,Y., Nakamura,Y., Suyama,A. and Sugano,S.		
	Diverse transcriptional Initiation revealed by fine, large-scale		
	mapping of mRNA start sites		
	EMBO Rep. 2 (5), 388-393 (2001)		
JOURNAL			

```

MEDLINE
COMMENT      21270072
              Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yusuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Source       Location/Qualifiers
            1..50
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             /note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"
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Best Local Similarity 81.5%; Pred.No. 8.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY           1 ATCAACCTGGCGAACAATGTCGAACCC 27
              1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db           35 ACCAGCCTGCAGCAACATGTCGAACCC 9
RESULT 12
AU102530/c   AU102530          50 bp    mRNA         linear     EST 30-Aug-2001
LOCUS        AU102530 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION   HS102245, mRNA sequence.
ACCESSION    AU102530
VERSION      AU102530.1 GI:3552050
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE    1 (bases 1 to 50)
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
              ,H., Ota,T., Isegaki,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
              ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
COMMENT      Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yusuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Source       Location/Qualifiers
            1..50
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             /clone="HS102245"
             /clone_lib="Sugano Homo sapiens cDNA library"
             /note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"
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ORIGIN
Query Match  63.3%; Score 19; DB 9; Length 50;
Best Local Similarity 81.5%; Pred.No. 8.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY           1 ATCAACCTGGCGAACAATGTCGAACCC 27

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Db 41 ACCAGCATGGCCACATGTCGAACCC 15

RESULT 13  
LOCUS AU102535/c 50 bp mRNA linear EST 30-AUG-2001  
DEFINITION AU102535 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
NBLAN362NF, mRNA sequence.  
ACCESSION AU102535  
VERSION AU102535  
KEYWORDS  
SOURCE EST.  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata  
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

TITLE  
JOURNAL MEDLINE  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yszukie@ms.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
, S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
source  
1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="NBLAN362NF"  
/note="Differential display comparison of untreated and  
dimethylflumurate treated U937 cells"

BASE COUNT  
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Query Match 63.3%; Score 19; DB 9; Length 50;  
Best Local Similarity 81.5%; Pred. No. 8.3e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ATCACTCTGGCGAATGTCGAACCC 27  
Db 38 ACCAGCTTGGCCACATGTCGAACCC 12

RESULT 14  
LOCUS AU102667/c 50 bp mRNA linear EST 30-AUG-2001  
DEFINITION AU102667 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
ADKA03070, mRNA sequence.  
ACCESSION AU102667  
VERSION AU102667  
KEYWORDS  
SOURCE EST.  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata  
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

TITLE  
JOURNAL MEDLINE  
COMMENT Contact: Yutaka Suzuki

Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yszukie@ms.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
, S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
source  
1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/note="Differential display comparison of untreated and  
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BASE COUNT  
ORIGIN 9 a 13 c 14 g 14 t

Query Match 63.3%; Score 19; DB 9; Length 50;  
Best Local Similarity 81.5%; Pred. No. 8.3e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ATCACTCTGGCGAATGTCGAACCC 27  
Db 29 ACCAGCTTGGCCACATGTCGAACCC 3

RESULT 15  
LOCUS AU103194/c 50 bp mRNA linear EST 30-AUG-2001  
DEFINITION AU103194 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
NBLAN2977NF, mRNA sequence.  
ACCESSION AU103194  
VERSION AU103194  
KEYWORDS  
SOURCE EST.  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)  
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata  
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki  
, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

TITLE  
JOURNAL MEDLINE  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yszukie@ms.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano  
, S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
source  
1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="NBLAN2977NF"  
/note="Differential display comparison of untreated and  
dimethylflumurate treated U937 cells"

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ORIGIN 10 a 8 c 14 g 18 t

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Best Local Similarity 81.5%; Pred. No. 8.3e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ATCACTCTGGCGAATGTCGAACCC 27  
Db 47 ACCAGCTTGGCCACATGTCGAACCC 21

Search completed: June 21, 2003, 23:58:55  
Job time : 1299.03 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 281.094 Seconds  
(without alignments)  
1449.478 Million cell updates/sec

Title: US-09-964-666-12

Perfect score: 14

Sequence: 1 CACTGCACTTCCA 14

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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41: em\_higo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	13	92.9	25	6	AR071993
2	12	85.7	27	6	I06372
3	11.4	81.4	20	6	AR193144
4	11.4	81.4	31	6	AR154129
5	11.4	81.4	36	6	AR077368
6	11.4	81.4	36	6	AR077405
7	11.4	81.4	36	6	AR117988
8	11.4	81.4	36	6	I95709
9	11	78.6	20	6	AX294160
10	11	78.6	20	6	AX296756
11	11	78.6	24	6	AX289527
12	11	78.6	24	6	AX292123
13	11	78.6	47	6	AX378274
14	10.4	74.3	18	6	AR049979
15	10.4	74.3	18	6	AR182515
16	10.4	74.3	20	6	AR158847
17	10.4	74.3	20	6	AR158848
18	10.4	74.3	20	6	AR158849
19	10.4	74.3	20	6	AR158850
20	10.4	74.3	20	6	AR158851
21	10.4	74.3	20	6	AR158852
22	10.4	74.3	20	6	AR158853
23	10.4	74.3	20	6	AR158854
24	10.4	74.3	20	6	AR173023
25	10.4	74.3	21	6	AR000120
26	10.4	74.3	21	6	AR205963
27	10.4	74.3	22	6	AR083596
28	10.4	74.3	22	6	AR110255
29	10.4	74.3	22	6	AX467734
30	10.4	74.3	25	6	AX042456
31	10.4	74.3	29	6	BD013007
32	10.4	74.3	29	23	BD010040
33	10.4	74.3	30	7	PEDFRGEMNY
34	10.4	74.3	36	6	A07187
35	10.4	74.3	36	6	E59618
36	10.4	74.3	36	6	I05106
37	10.4	74.3	36	6	I07406
38	10.4	74.3	36	6	I07637
39	10.4	74.3	36	6	I71445
40	10.4	74.3	41	6	AR077392
41	10.4	74.3	41	6	AR077493
42	10.4	74.3	41	6	AR118012
43	10.4	74.3	41	6	I95733
44	10.4	74.3	44	6	AR077636
45	10.4	74.3	45	6	AX201429

#### ALIGNMENTS

RESULT 1  
LOCUS AR071993/c 25 bp DNA  
DEFINITION Sequence 23 from patent US 5912168.  
ACCESSION AR071993  
VERSION AR071993.1 GI:7222881  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Watson,J.D. and Ruderf,F.  
TITLE CD95 regulatory gene sequences  
JOURNAL Patent: US 5912168-A 23 15-JUN-1999;  
FEATURES Location/Qualifiers

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/organism="unknown"  
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OY: 1 CACTGCACCTTNCCA 14  
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Db 23 CACTGCACCTTACCA 10

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LOCUS 106372  
DEFINITION Sequence 33 from Patent EP 0293934.  
ACCESSION 106372  
VERSION 106372.1 GI:590632  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Mulvihill,E.R., Nexo,B.A., Yoshitake,S., Ikeda,Y., Suzuki,S.,  
TITLE Hashimoto,A. and Yuzuriha,T.  
JOURNAL Mutant t-PA with kringles replacement  
FEATURES Patent: EP 0293934-A1 33 07-DEC-1988;  
Location/Qualifiers  
source 1. .27  
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ORIGIN

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Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY: 1 CACTGCACCTTNCC 13  
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Db 15 CACTGCACCTTCCC 27

RESULT 3  
LOCUS AR193144  
DEFINITION Sequence 29 from patent US 6346416.  
ACCESSION AR193144  
VERSION AR193144.1 GI:20239109  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dean,N.M. and Cowseert,L.M.  
TITLE Antisense inhibition of HPK/GCK-like kinase expression  
JOURNAL Patent: US 6346416-A 29 12-FEB-2002;  
FEATURES Location/Qualifiers  
source 1. .20  
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BASE COUNT 3 a 7 c 4 g 6 t  
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Query Match 81.4%; Score 11.4; DB 6; Length 20;  
Best Local Similarity 85.7%; Pred. No. 1.9e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY: 1 CACTGCACCTTNCCA 14  
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Db 1 CACTGCATTTTCCA 14

RESULT 4  
LOCUS AR154129  
DEFINITION Sequence 7 from patent US 6238866.  
ACCESSION AR154129  
VERSION AR154129.1 GI:15122182  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Yeh,H.R. and Wlck,C.H.  
TITLE Detector for nucleic acid typing and methods of using the same  
JOURNAL Patent: US 6238866-A 7 29-MAY-2001;  
FEATURES Location/Qualifiers  
source 1. .31  
/organism="unknown"

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Best Local Similarity 85.7%; Pred. No. 1.9e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY: 1 CACTGCACCTTNCCA 14  
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Db 9 CACTGTACTTCCCA 22

RESULT 5  
LOCUS AR077368  
DEFINITION Sequence 83 from patent US 5962255.  
ACCESSION AR077368  
VERSION AR077368.1 GI:10004114  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 36)  
AUTHORS Griffiths,A.David., Williams,S.Cameron., Waterhouse,P.Michael.,  
TITLE Nissim,A., Winter,G.Paul., Johnson,K.Stuart. and  
JOURNAL Smith,A.John.Hammond.  
FEATURES Methods for producing recombinant vectors  
Patent: US 5962255-A 83 05-OCT-1999;  
Location/Qualifiers  
source 1. .36  
/organism="unknown"

BASE COUNT 10 a 13 c 7 g 6 t  
ORIGIN

Query Match 81.4%; Score 11.4; DB 6; Length 36;  
Best Local Similarity 85.7%; Pred. No. 1.9e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY: 1 CACTGCACCTTNCCA 14  
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Db 9 CACTGCACCTTGCCA 22

RESULT 6  
LOCUS AR077405  
DEFINITION Sequence 120 from patent US 5962255.  
ACCESSION AR077405  
VERSION AR077405.1 GI:10004151  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 36)  
AUTHORS Griffiths,A.David., Williams,S.Cameron., Waterhouse,P.Michael.,  
TITLE Nissim,A., Winter,G.Paul., Johnson,K.Stuart. and

Griffiths,A.David., Williams,S.Cameron., Waterhouse,P.Michael.,  
Nissim,A., Winter,G.Paul., Johnson,K.Stuart. and





LOCUS AX289527 24 bp DNA linear PAT 21-NOV-2001  
DEFINITION Sequence 1289 from Patent WO0179548.  
ACCESSION AX289527  
VERSION AX289527.1 GI:17051210  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kliman,R.  
TITLE Method of designing addressable array for detection of nucleic acid  
JOURNAL sequence differences using ligase detection reaction  
PATENT: WO 0179548-A 1289 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)  
FEATURES  
source 1..24  
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/db\_xref="taxon:32630"  
/note="Hypothetical Probe Sequence"  
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Best Local Similarity 91.7%; Pred. No. 3.5e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 22 CTGCACTTGCA 11  
RESULT 12  
LOCUS AX292123 24 bp DNA linear PAT 21-NOV-2001  
DEFINITION Sequence 3885 from Patent WO0179548.  
ACCESSION AX292123  
VERSION AX292123.1 GI:17053806  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kliman,R.  
TITLE Method of designing addressable array for detection of nucleic acid  
JOURNAL sequence differences using ligase detection reaction  
PATENT: WO 0179548-A 3885 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)  
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/note="Hypothetical Probe Sequence"  
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Best Local Similarity 91.7%; Pred. No. 3.5e+04;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CACTGCCTTNC 12  
Db 16 CACTGCCTTGC 5  
RESULT 13  
LOCUS AX378274 47 bp DNA linear PAT 18-MAR-2002  
DEFINITION Sequence 63 from Patent WO0206525.  
ACCESSION AX378274  
VERSION AX378274.1 GI:19574124  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1  
AUTHORS Cohen,D., Blumenfeld,M., Chumakov,I., Abderrahim,H. and Bihain,B.  
TITLE Obesity associated diallelic marker maps  
JOURNAL Patent: WO 0206525-A 63 24-JAN-2002;  
GENSET (FR)  
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variation 24  
/note="99-28363-114 : polymorphic base A or G"  
BASE COUNT 9 a 8 c 15 g 14 t 1 others  
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Best Local Similarity 78.6%; Pred. No. 3.6e+04;  
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CACTGCCTTNC A 14  
Db 32 CACTGCAGTTCCA 19  
RESULT 14  
LOCUS AR049979 18 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 2 from patent US 5824794.  
ACCESSION AR049979  
VERSION AR049979.1 GI:5971971  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Borden,P.Ann. and Heller,R.Anand.  
TITLE Human stromelysin-1 promoter  
JOURNAL Patent: US 5824794-A 2 20-OCT-1998;  
FEATURES  
source 1..18  
/organism="unknown"  
BASE COUNT 2 a 9 c 1 g 6 t  
ORIGIN  
Query Match 74.3%; Score 10.4; DB 6; Length 18;  
Best Local Similarity 84.6%; Pred. No. 8.9e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CACTGCCTTNC 13  
Db 3 CACTGCCCTTACC 15  
RESULT 15  
LOCUS AR182515 18 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 2 from patent US 6338944.  
ACCESSION AR182515  
VERSION AR182515.1 GI:20225722  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Borden,P.Ann. and Heller,R.Anand.  
TITLE Methods for measuring stromelysin-1 promoter activity  
JOURNAL Patent: US 6338944-A 2 15-JAN-2002;  
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BASE COUNT 2 a 9 c 1 g 6 t  
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Query Match 74.3%; Score 10.4; DB 6; Length 18;  
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 Db 3 CACTGCCCTTACC 15

Search completed: June 21, 2003, 22:14:35  
 Job time : 284.094 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:51 ; Search time 76.7812 Seconds  
(without alignments)  
410.621 Million cell updates/sec

Title: US-09-964-666-12  
Perfect score: 14  
Sequence: 1 CACTGCACCTTCCA 14

Scoring table: IDENTITY\_NTC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	13	92.9	27	20	AAV23155
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C 4	11.4	81.4	22	22	AAV23155
C 5	11.4	81.4	27	9	AAV23155
C 6	11.4	81.4	27	9	AAV23155
C 7	11.4	81.4	31	22	AAV23155
C 8	11.4	81.4	36	14	AAV23155
C 9	11.4	81.4	41	22	AAV23155

C 10	11	78.6	20	21	AAV23155	Dog genomic marker
C 11	11	78.6	20	24	AB194202	Capture oligonucleotide
C 12	11	78.6	20	24	AB196798	Capture oligonucleotide
C 13	11	78.6	24	24	AB184974	Capture oligonucleotide
C 14	11	78.6	24	24	AB184975	Capture oligonucleotide
C 15	11	78.6	24	24	AB190166	Capture oligonucleotide
C 16	11	78.6	24	24	AB190167	Capture oligonucleotide
C 17	11	78.6	28	21	AAV21469	Human PA12 PCR pri
C 18	11	78.6	47	24	ABK40815	Human obesity-asso
C 19	10.6	75.7	31	20	AAV20147	Human biallelic po
C 20	10.4	74.3	13	23	ABH25832	Oligonucleotide SE
C 21	10.4	74.3	13	23	ABH25833	Oligonucleotide SE
C 22	10.4	74.3	17	20	AAV90213	Human yes1 biallel
C 23	10.4	74.3	18	19	AAV62716	Nucleotide sequenc
C 24	10.4	74.3	18	21	AAV73123	Human biallelic ma
C 25	10.4	74.3	18	24	ABH92015	Human stromelysin-
C 26	10.4	74.3	20	16	AAV95921	Primer A (Group 13
C 27	10.4	74.3	20	22	AAV10648	Human caspase 3 an
C 28	10.4	74.3	20	22	AAH80505	Oligonucleotide hy
C 29	10.4	74.3	20	22	AAH80506	Oligonucleotide hy
C 30	10.4	74.3	20	22	AAH80507	Oligonucleotide hy
C 31	10.4	74.3	20	22	AAH80508	Oligonucleotide hy
C 32	10.4	74.3	20	22	AAH80509	Oligonucleotide hy
C 33	10.4	74.3	20	22	AAH80510	Oligonucleotide hy
C 34	10.4	74.3	20	22	AAH80511	Oligonucleotide hy
C 35	10.4	74.3	20	22	AAH80512	Oligonucleotide hy
C 36	10.4	74.3	20	22	AAH63063	Shrimp white spot
C 37	10.4	74.3	20	24	ABK14343	Human interleukin-
C 38	10.4	74.3	21	17	AAV34465	Primer used in alc
C 39	10.4	74.3	21	17	AAV34465	Human arylsulphata
C 40	10.4	74.3	21	21	AAH49891	Zs1966 sequencing
C 41	10.4	74.3	21	21	AAH73538	Human GPR21 DNA P
C 42	10.4	74.3	21	22	AAH25541	PCR primer used to
C 43	10.4	74.3	21	24	ABH35625	Nicotiana benthami
C 44	10.4	74.3	22	20	AAV28746	Primer RT-R6 for d
C 45	10.4	74.3	22	20	AAV45623	PCR primer RT-R6 f

## ALIGNMENTS

RESULT 1  
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ID AAV23155 standard; DNA; 25 BP.  
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AC AAV23155;  
XX  
DT 23-JUL-1998 (first entry)  
XX  
DE Primer -1299/-1/CAT for human CD95 gene.  
XX  
KW CD95; regulatory region; silencer; enhancer; apoptosis; inhibitor;  
KW cancer; viral infection; neurodegeneration; autoimmune disease; human;  
KW gene therapy; transcription factor; PCR primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9808965-A2.  
XX  
PD 05-MAR-1998.  
XX  
PF 29-AUG-1997; 97WO-NZ00107.  
XX  
PR 30-AUG-1996; 96US-0713557.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
PI Rudert F, Watson JD;  
XX  
DR WPI; 1998-179445/16.  
XX  
PT New regulatory regions from the CD95 gene and transcription factors

PT that interact with them - for control of apoptosis, e.g. in  
PT treatment of cancer, viral infection, neurodegeneration and  
PT auto-immune disease  
XX  
PS Disclosure; Page 40; 60pp; English.  
XX  
CC This sequence is a primer for the CD95 gene, and is used to isolate the  
CC regulatory nucleic acids of the invention. The regulatory regions  
CC (silencers or enhancers) are involved in apoptosis, e.g. inhibition of  
CC CD95 expression will inhibit apoptosis. Regulation of apoptosis is useful  
CC in treatment of cancer, (retroviral infection, neurodegeneration and  
CC autoimmune disease, e.g. by gene therapy for expressing transcription  
CC factors or expression of antisense sequences to inhibit transcription  
CC factor production. The regulatory nucleic acids and transcription factors  
CC are also useful for studying regulation of CD95 in vitro or in vivo, to  
CC screen for modulators and as probes to isolate related genes.  
XX  
SO Sequence 25 BP; 6 A; 4 C; 9 G; 6 T; 0 other;  
Query Match 92.9%; Score 13; DB 19; Length 25;  
Best Local Similarity 92.9%; Pred. No. 3.6e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CACTGCACCTTNCCA 14  
Db 23 CACTGCACCTTACCA 10  
IIIIIIIIIIII  
IIIIIIIIIIII  
RESULT 2  
AAx84455/c  
ID AAx84455 standard; DNA: 27 BP.  
XX  
AC AAx84455;  
XX  
DT 10-SEP-1999 (first entry)  
XX  
DE PCR primer for BCNG coding sequence.  
XX  
XX BCNG; brain cyclic nucleotide gated ion channel; epilepsy; hyperalgesia;  
XX Alzheimer's Disease; Parkinson's Disease; long QT syndrome; dyslexia;  
XX sick sinus syndrome; age-related memory loss; cystic fibrosis;  
XX sudden death syndrome; pacemaker rhythm dysfunction; sensory disorder;  
XX auditory disorder; respiratory disorder; attention deficit disorder;  
XX learning disability; drug addiction; therapy; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
XX WO9932615-A1.  
XX  
PD 01-JUL-1999.  
XX  
PF 23-DEC-1998; 98WO-US27630.  
XX  
PR 28-MAY-1998; 98US-0086436.  
XX  
PR 23-DEC-1997; 97US-0997685.  
XX  
XX (UYCO ) UNIV COLUMBIA NEW YORK.  
XX  
XX PA  
XX PI Bartsch D, Grant S, Kandel ER, Santoro B, Siegelbaum S;  
XX PI Tibbs G;  
XX DR WPI; 1999-418922/35.  
XX  
XX An isolated nucleic acid encoding a brain or heart cyclic  
XX nucleotide-gated ion channel  
XX  
PS Claim 24; Page 205; 213pp; English.  
XX  
XX This sequence is a PCR primer for DNA encoding the brain cyclic  
XX nucleotide-gated ion channel (BCNG) of the invention. BCNG and  
XX BCNG-related proteins are useful in screening for compounds that  
XX modulate, interact or affect expression. Compounds, e.g. antagonists and  
XX agonists, identified in the methods are useful for modulating BCNG or

CC BCNG-related protein activity. Modulation is increased or decreased ion  
CC permissivity or ion flow rate. Modulators of BCNG can be used to treat a  
CC neurological, renal, pulmonary, hepatic or cardiovascular condition. Such  
CC conditions include epilepsy, Alzheimer's Disease, Parkinson's Disease,  
CC long QT syndrome, sick sinus syndrome, age-related memory loss, cystic  
CC fibrosis, sudden death syndrome or pacemaker rhythm dysfunction. BCNG or  
CC BCNG-related protein can also be used to treat sensory disorders,  
CC e.g. blindness, loss of vision, loss of smell, numbness and lack of  
CC ability to taste. Also treatable are auditory disorders, respiratory  
CC disorders due to defects in central nervous system areas that control  
CC respiration or defects in the lungs, dyslexia, attention deficit disorder  
CC or learning disabilities, drug addiction and regulation of cell  
CC secretions. The proteins are useful targets for screening for drugs that  
CC are effective in the control of pain and hyperalgesia.  
XX  
SO Sequence 27 BP; 6 A; 7 C; 9 G; 5 T; 0 other;  
Query Match 92.9%; Score 13; DB 20; Length 27;  
Best Local Similarity 92.9%; Pred. No. 3.6e+02;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CACTGCACCTTNCCA 14  
Db 21 CACTGCACCTTGCCA 8  
IIIIIIIIIIII  
IIIIIIIIIIII  
RESULT 3  
ABK44429  
ID ABK44429 standard; DNA: 20 BP.  
XX  
AC ABK44429;  
XX  
DT 05-JUN-2002 (first entry)  
XX  
DE Human HPR/GCK-like kinase antisense oligonucleotide, ISIS 105328.  
XX  
XX Human: HPR/GCK-like kinase; antiinflammatory; cytostatic; antimicrobial;  
XX HKK; NIK; Nck-interacting kinase; infection; inflammation; tumour;  
XX antisense gene therapy; antisense oligonucleotide; ss.  
XX  
OS Homo sapiens.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX FH modified\_base 1..5  
XX FT /\*tag= a  
XX FT /mod\_base= OTHER  
XX FT /note= "Optionally 2'-methoxyethyl (2'WOE) nucleotides"  
XX FT modified\_base 1..20  
XX FT /\*tag= b  
XX FT /mod\_base= OTHER  
XX FT /note= "Phosphorothioate backbone; all cytidines  
XX FT modified\_base 16..20  
XX FT /\*tag= c  
XX FT /mod\_base= OTHER  
XX FT /note= "Optionally 2'-methoxyethyl (2'WOE) nucleotides"  
XX  
XX PN US6346416-B1.  
XX  
XX 12-FEB-2002.  
XX  
XX PD 29-AUG-2000; 2000US-0651011.  
XX  
XX PF 29-AUG-2000; 2000US-0651011.  
XX  
XX PR (ISIS-) ISIS PHARM INC.  
XX  
XX PA  
XX XX  
XX PI Dean NM, Cowsett LM;  
XX PI WPI; 2002-237091/29.  
XX  
XX New antisense compound, useful for preventing or delaying infection,

PT inflammation or tumour formation, is targeted to nucleic acid molecule  
 PT encoding HPK/GCK-like kinase (HGK) and hybridises and inhibits HGK  
 PT expression  
 PS Claim 14: Column 43-44; 37pp; English.  
 XX  
 CC The invention relates to an antisense compound (I) of 8-50 nucleobases in  
 CC length targeted to a start codon region, coding region or 3'-untranslated  
 CC region of a nucleic acid molecule encoding HPK/GCK (undefined)-like  
 CC kinase (HGK) (also known as NIK for NIK-interacting kinase), which  
 CC specifically hybridises with and inhibits expression of HGK. (I) is  
 CC useful for inhibiting the expression of HPK/GCK-like kinase in cells or  
 CC tissues in vitro. (I) is useful prophylactically e.g. to prevent or delay  
 CC infection, inflammation and tumour formation. (I) is also useful as a  
 CC diagnostic and research reagent. (I) is also useful for distinguishing  
 CC functions of various members of a biological pathway and in  
 CC antisense gene therapy. The present sequence represents an antisense  
 CC oligonucleotide targeted to human HPK/GCK-like kinase.  
 CC  
 SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 other;  
 XX  
 OY Query Match 81.4%; Score 11.4; DB 24; Length 20;  
 Best Local Similarity 85.7%; Pred. No. 3e+03;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 DB 1 CACTGCACCTTNCCA 14  
 1 CACTGCACCTTNCCA 14  
 RESULT 4  
 AAS03611  
 ID AAS03611 standard; DNA; 22 BP.  
 XX  
 AC AAS03611;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE PCR primer rend9b1, used to detect RHD positive haplotypes.  
 XX  
 KW Rhesus box; RHD positive; sequence length polymorphism: SSP; RHD; SMP1;  
 KW RHCE; RHD negative; blood group typing; blood transfusion; antigen C;  
 KW haemolytic disease of the newborn; chromosome 1 p34.1.p36; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200132702-A2.  
 XX  
 PA 10-MAY-2001.  
 PD  
 PF 31-OCT-2000; 2000MO-EP10745.  
 XX  
 PR 02-NOV-1999; 99EP-0121686.  
 XX  
 PR 31-MAY-2000; 2000EP-0111696.  
 XX  
 PA (DRKB-) DRK BLUTSPENDEDIENST BADEN WÜRTTEMBERG.  
 XX  
 PI Flegel WA, Wagner FF;  
 XX  
 DR WPI; 2001-291052/30.  
 XX  
 PT New nucleic acid molecular structure, useful for detection of common  
 PT RHD positive haplotypes in D-negative individuals, comprises RHD, SMP1  
 PT and RHCE genes  
 XX  
 PS Example 13; Page 56; 135pp; English.  
 XX  
 CC The sequence represents PCR primer rend9b1, used to detect RHD positive  
 CC haplotypes in RHD negative individuals. The primer was used in DNA  
 CC typing using PCR-sequence length polymorphism (SSP) of the Rhesus genes  
 CC locus comprising the RHD, SMP1 and RHCE (all undefined) genes and/or the  
 CC Rhesus box(es), preferably the hybrid Rhesus box, the upstream Rhesus box  
 CC and/or the downstream Rhesus box. The RHD and RHCE genes are located at

CC chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the  
 CC RHD deletion in the common RHD negative haplotypes. The primers of the  
 CC invention are useful for: (1) the specific detection of the common RHD  
 CC positive haplotypes in D-negative individuals; (2) blood group typing;  
 CC (3) determining whether a patient can be transfused with Rhd negative  
 CC blood and whether blood is suitable for transfusion to patients who  
 CC should not be exposed to antigen C; (4) assessing the risk of a Rhd  
 CC negative mother of conceiving or carrying an Rhd positive foetus. Anti-D  
 CC antibodies are useful for treating pregnant women who are Rhesus D  
 CC negative, where the foetus is not homozygous for the RHD gene to treat  
 CC or prevent haemolytic disease of the newborn.  
 CC  
 SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;  
 XX  
 OY Query Match 81.4%; Score 11.4; DB 22; Length 22;  
 Best Local Similarity 85.7%; Pred. No. 3.1e+03;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 DB 1 CACTGCACCTTGACA 14  
 1 CACTGCACCTTNCCA 14  
 1 CACTGCACCTTGACA 14  
 RESULT 5  
 AAN81248  
 ID AAN81248 standard; DNA; 27 BP.  
 XX  
 AC AAN81248;  
 XX  
 DT 14-SEP-1990 (first entry)  
 XX  
 DE Probe 0-YNH24 to identify intrinsic polymorphism of loci in human DNA.  
 XX  
 KW Synthetic probe; restriction fragment length polymorphism;  
 KW paternity testing; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN EP294098-A.  
 PD  
 PD 07-DEC-1988.  
 XX  
 XX 26-MAY-1988; 88EP-0304763.  
 PF  
 PR 17-MAY-1988; 88US-019482.  
 XX  
 PA (CITY ) CITY OF HOPE MED CENTRE.  
 XX  
 PI Wallace RB;  
 XX  
 DR WPI; 1988-347751/49.  
 XX  
 PT New oligonucleotide hybridisation probe specific for repeat units  
 PT with high specificity for single locus, useful e.g. in paternity testing.  
 XX  
 PS Claim 7(e); Page 6; 9pp; English.  
 XX  
 CC Total length: 27.  
 CC Length repeat unit: 31.  
 CC No. repeat units: 1.  
 CC Category of hybridisation to human DNA: 1.  
 CC The probe is complementary to one or two repeat units of VTNR loci.  
 CC The probe is used for genetic identification of a sample of human  
 CC genomic DNA, eg for paternity testing, diagnosing cancer or genetic  
 CC diseases, and studying post-bone marrow transplant chimerism. Under high  
 CC criteria, it yields a locus-specific or multi-loci, polymorphic  
 CC hybridisation pattern, and is more specific for a single locus (or small  
 CC no. of loci) than known probes.  
 CC See also N981243-53.  
 XX  
 SQ Sequence 27 BP; 7 A; 12 C; 2 G; 6 T; 0 other;  
 XX  
 OY Query Match 81.4%; Score 11.4; DB 9; Length 27;

Best Local Similarity 85.7%; Pred. No. 3.1e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACCTTNCCA 14  
14 CACTGACTTCCCA 27

## RESULT 6

AA82045  
ID AAN82045 standard; DNA: 27 BP.

AC AAN82045;

DT 12-DEC-1990 (first entry)

DE Probe O-YNH24 for human genomic DNA.

KW Synthetic oligonucleotide; probe O-YNH24; ss DNA; human genomic DNA.

PN EP294098-A.

PD 07-DEC-1998.

PF 26-MAY-1988; 88EP-0304763.

PR 29-MAY-1987; 87US-0055224.

PR 17-MAY-1988; 88US-0194982.

PA (CITY ) CITY OF HOPE.

PI Wallace RB;

DR WPI; 1988-34751/49.

PT New Oligonucleotide hybridisation probe specific for repeat units -

PT with high specificity for single locus, useful e.g. in paternity

PS Claim 7; page 6; 8pp; English.

CC The probe is used for genetic identification of a sample of human genomic  
CC DNA, e.g. for paternity testing, diagnosing cancer or genetic diseases,  
CC and studying bone marrow transplant chimerism. Under high criteria it  
CC yielded locus-specific or multi-loci, polymorphic hybridisation pattern,  
CC and is more specific for a single locus (or small number of loci) than  
CC known probes.

SQ Sequence 27 BP; 7 A; 12 C; 2 G; 6 T; 0 other;

Query Match 81.4%; Score 11.4; DB 9; Length 27;

Best Local Similarity 85.7%; Pred. No. 3.1e+03;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACCTTNCCA 14  
14 CACTGACTTCCCA 27

## RESULT 7

AA504026  
ID AAS04026 standard; DNA: 31 BP.

AC AAS04026;

DT 12-SEP-2001 (first entry)

DE VNTR hybridisation probe; minisatellite YNH24.

KW Human: probe: hypervariable number of tandem repeat: VNTR;

KW species identification; virus detection; minisatellite YNH24;

KW Epstein-Barr virus; ds.

OS Homo sapiens.

FX Key Location/Qualifiers

FT modified\_base 31

FT /\*tag= a /note= "labelled with 4'-6-diamidino-2-phenylindole"

PN US6238866-BI.

PD 29-MAY-2001.

PF 08-FEB-1999; 99US-0246277.

PR 16-APR-1996; 96US-0015965.

PR 16-APR-1997; 97US-0838157.

PA (USSA ) US SEC OF ARMY.

PI Yeh HR, Wick CH;

DR WPI; 2001-366471/38.

PT New device with a panel of double stranded oligonucleotide probes  
PT immobilized on a solid support, useful for detecting or characterizing  
PT a nucleic acid analyte without requiring electrophoresis or the direct  
PT sequencing of analyte

PS Example 1; Column 20; 24pp; English.

CC The sequence represents the nucleotide sequence of variable number of  
CC tandem repeats (VNTR) hybridisation probe, minisatellite YNH24. The  
CC sequence was used as a probe to demonstrate the method of the invention,  
CC which is a device for detecting or characterizing a nucleic acid  
CC analyte. The device comprises a panel of double stranded oligonucleotide  
CC probes immobilised on a solid support. Each probe has a first strand  
CC comprising a hypervariable number of tandem repeat sequences and a second  
CC strand complementary to the first strand. The probe is selected to  
CC hybridise to at least one allele of the nucleic acid analyte and  
CC comprises a fragment of an Epstein-Barr virus genome spanning from  
CC nucleotide 7421-8042. The device is useful for detecting or  
CC characterising a nucleic acid analyte without requiring electrophoresis  
CC or the direct sequencing of analyte samples or analyte fragments. The  
CC device is particularly useful for individual and species identification.  
CC The device is simple and reliable compared to those previously used in  
CC prior methods. The device is also readily applied outside of a laboratory  
CC environment, such as detection of pathogenic virus strains under  
CC emergency conditions in the field.

SQ Sequence 31 BP; 7 A; 14 C; 3 G; 7 T; 0 other;

Query Match 81.4%; Score 11.4; DB 22; Length 31;

Best Local Similarity 85.7%; Pred. No. 3.2e+03;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACCTTNCCA 14  
9 CACTGACTTCCCA 22

## RESULT 8

AAQ49016  
ID AAQ49016 standard; DNA: 36 BP.

AC AAQ49016;

DT 22-APR-1994 (first entry)

DE Multimeric (SBP) antibody chain primer.

KW SBP; specific binding pair members; antibody; RCDP;

KW replicable genetic display package; recombination; PCR;

KW polymerase chain reaction; ss.



OS Synthetic.  
 XX WO9319172-A.  
 XX 30-SEP-1993.  
 XX  
 XX 24-MAR-1993; 93WO-GB00605.  
 XX  
 XX 24-MAR-1992; 92GB-0006318.  
 PR 15-MAY-1992; 92MO-GB00883.  
 XX  
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
 PA (MEDI-) MEDICAL RES. COUNCIL.  
 XX  
 XX Griffiths AD, Johnson KS, Smith AJH, Waterhouse P;  
 PI Winter GP;  
 DR WPI: 1993-320739/40.  
 XX  
 XX Prodn. of specific binding pair members, e.g. antibody chains -  
 PT by display on surface of replicable genetic display packages  
 XX  
 XX Disclosure: Page 58; 81pp; English.  
 PS  
 CC The primers (AAQ48987-Q49045) are used in the amplification of Kappa  
 CC and lambda-chain genes of various antibodies. These genes are then  
 CC recombed into the same replicon, resulting in very diverse libraries  
 CC of antibody chains, e.g. from unimmunised donors. It is also useful  
 CC for chain shuffling, mutagenesis, humanising and CDR imprinting.  
 XX  
 XX Sequence 36 BP; 10 A; 13 C; 7 G; 6 T; 0 other;  
 SQ

Query Match 81.4%; Score 11.4; DB 14; Length 36;  
 Best Local Similarity 85.7%; Pred. No. 3.3e+03;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACTGCACCTTCCA 14  
 |||||||  
 DB 9 CAGTGCACCTGCCA 22

RESULT 9  
 AAH46243  
 ID AAH46243 standard; DNA; 41 BP.  
 XX  
 AC AAH46243;  
 XX  
 DT 25-SEP-2001 (first entry)  
 XX  
 DE Human neuronal thread protein 17 probe, SEQ ID NO:8.  
 XX  
 KW Human neuronal thread protein 17; recombinant production;  
 KW malignant tumour; cancer; blood disease; HIV infection;  
 KW human immunodeficiency virus; immune disorder; inflammatory condition;  
 KW cytostatic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200146237-A1.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PF 18-DEC-2000; 2000MO-CN00585.  
 XX  
 PR 22-DEC-1999; 99CN-0125691.  
 XX  
 XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
 PA  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI: 2001-441667/47.  
 XX  
 PT Human neuronal thread protein 17 and encoded polynucleotide, applicable

PT in diagnosis and treatment of cancer, hemopathy, HIV infection,  
 PT immunological diseases and phlogosis  
 XX  
 XX Example 7; Page 17; 40pp; Chinese.  
 PS  
 CC The invention relates to human neuronal thread protein 17 (AAB98894),  
 CC nucleic acids encoding it (AAH46238), and a method for the recombinant  
 CC production of the protein. The present invention additionally discloses  
 CC an antagonist of neuronal thread protein 17 for therapeutic use, and an  
 CC antibody which specifically binds to neuronal thread protein 17. Neuronal  
 CC thread protein 17, and nucleotides which encode it may be used for  
 CC treating a variety of diseases, such as malignant tumours, blood  
 CC diseases, HIV (human immunodeficiency virus) infection, immune disorders  
 CC and inflammatory conditions. The protein may also be used to screen for  
 CC modulators of its activity or for peptide fingerprinting identification.  
 CC The polynucleotide can be used as a primer for nucleic acid amplification  
 CC reactions or as a probe for hybridisation reactions, or in producing gene  
 CC chips or microarrays. Sequences AAH46243-AAH46244 represent human  
 CC neuronal thread protein 17 probes used in an exemplification of the  
 CC invention.  
 XX  
 XX Sequence 41 BP; 9 A; 12 C; 10 G; 10 T; 0 other;  
 SQ

Query Match 81.4%; Score 11.4; DB 22; Length 41;  
 Best Local Similarity 85.7%; Pred. No. 3.3e+03;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACTGCACCTTCCA 14  
 |||||||  
 DB 28 CACTGCACCTTCCA 41

RESULT 10  
 AA66165  
 ID AA66165 standard; DNA; 20 BP.  
 XX  
 AC AA66165;  
 XX  
 DT 09-OCT-2000 (first entry)  
 XX  
 DE Dog genomic marker oligonucleotide sequence SEQ ID NO:27.  
 XX  
 KW Dog; genome; genomic marker; radiation hybrid map; identification;  
 KW chromosome location; gene marker; polymorphic microsatellite marker;  
 KW phenotype; behaviour; pedigree; ss.  
 XX  
 OS Canis familiaris.  
 XX  
 PN WO200029615-A2.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 15-NOV-1999; 99WO-IB01907.  
 XX  
 PR 13-NOV-1998; 98US-0108193.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Galibert F, Andre C;  
 XX  
 DR WPI: 2000-387821/33.  
 XX  
 PT New radiation hybrid map of the dog, Canine familiaris, genome, useful  
 PT for e.g. identifying genes implicated in phenotypic and behavioral  
 PT traits or in genetic diseases and for studying dog pedigrees  
 XX  
 PS Claim 1; Page 54; 87pp; English.  
 XX  
 CC The present invention describes a radiation hybrid map of the dog  
 CC (Canine familiaris) genome comprising the genome location of a marker  
 CC selected from AA66139 to AA66942. The radiation hybrid map is useful  
 CC for identifying and localising dog genes, since it covers approximately  
 CC 80 % of the dog genome and provides a dense map integrating different

CC types (i.e. Type I and Type II) of markers. The map and the dog genome  
CC markers (or complementary sequences) are especially useful to identify  
CC genes responsible for phenotypic and behavioural traits in dogs, to  
CC identify morbid genes, to analyse diseases and identify implicated genes  
CC in such diseases and their alleles, and to study dog pedigrees. They  
CC may also be useful for isolating corresponding human gene sequences  
CC e.g. genes involved in genetic diseases.  
XX  
SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 other;  
Query Match 78.6%; Score 11; DB 21; Length 20;  
Best Local Similarity 91.7%; Pred. No. 5.2e+03;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 2 ACTGCACCTTNC 13  
| | | | | | | | | | | | | |  
Db 9 ACTGCACCTTCCC 20  
RESULT 11  
ABI94202/c  
ID ABI94202 standard; DNA: 20 BP.  
AC ABI94202;  
XX  
DT 16-FEB-2002 (first entry)  
XX  
DE Capture oligonucleotide zip ID#1289 oligo #9.  
XX  
KW Human: K-ras; PCR primer; probe; capture probe; mutation detection;  
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;  
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;  
KW environmental monitoring; food industry; feed industry; ss.  
XX  
OS Synthetic.  
XX  
PN WO200179548-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 04-APR-2001; 2001WO-US10958.  
XX  
PR 14-APR-2000; 2000US-197271P.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Barany F, Zivvi M, Gerry NP, Favis R, Kilman R;  
XX  
DR WPI: 2002-034366/04.  
XX  
PT Designing capture oligonucleotide probes for use on a support to which  
XX complementary oligonucleotides hybridize with little mismatch -  
XX  
PS Example 5; Fig 29; 300pp; English.  
XX  
CC The present invention describes a method (M1) for designing capture  
CC oligonucleotide probes (I) for use on a support to which complementary  
CC oligonucleotide probes (II) will hybridise with little mismatch, where  
CC (I) have melting temperatures within a narrow range. The method is useful  
CC for detecting infectious diseases caused by bacterial infectious agents  
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal  
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
CC Epstein-Barr virus and polio virus, and parasitic infectious agents  
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus  
CC medinensis. The method is also useful for detecting genetic diseases such  
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.  
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
CC involved in DNA amplification, replication, recombination or repair, the  
CC cancer is specifically associated with a gene selected from BRCA1 gene,  
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
CC method is also used for environmental monitoring, forensics and the food

CC and feed industry, detecting comprises scanning (using e.g. a scanning  
CC electron microscope and infrared microscope) the support at the  
CC particular sites and identifying if ligation of the oligonucleotide probe  
CC sets occurred and correlating (using a computer) identified ligation to a  
CC presence or absence of the target nucleotide sequences. AB182074 to  
CC AB197546 represent oligonucleotide sequences used in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 other;  
Query Match 78.6%; Score 11; DB 24; Length 20;  
Best Local Similarity 91.7%; Pred. No. 5.2e+03;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 3 CTGCACCTTNC 14  
| | | | | | | | | | | | | |  
Db 18 CTGCACCTTGCCA 7  
RESULT 12  
ABI96798/c  
ID ABI96798 standard; DNA: 20 BP.  
AC ABI96798;  
XX  
DT 16-FEB-2002 (first entry)  
XX  
DE Capture oligonucleotide zip ID#3885 oligo #9.  
XX  
KW Human: K-ras; PCR primer; probe; capture probe; mutation detection;  
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;  
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;  
KW environmental monitoring; food industry; feed industry; ss.  
XX  
OS Synthetic.  
XX  
PN WO200179548-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 04-APR-2001; 2001WO-US10958.  
XX  
PR 14-APR-2000; 2000US-197271P.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Barany F, Zivvi M, Gerry NP, Favis R, Kilman R;  
XX  
DR WPI: 2002-034366/04.  
XX  
PT Designing capture oligonucleotide probes for use on a support to which  
XX complementary oligonucleotides hybridize with little mismatch -  
XX  
PS Example 5; Fig 29; 300pp; English.  
XX  
CC The present invention describes a method (M1) for designing capture  
CC oligonucleotide probes (I) for use on a support to which complementary  
CC oligonucleotide probes (II) will hybridise with little mismatch, where  
CC (I) have melting temperatures within a narrow range. The method is useful  
CC for detecting infectious diseases caused by bacterial infectious agents  
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal  
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
CC Epstein-Barr virus and polio virus, and parasitic infectious agents  
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus  
CC medinensis. The method is also useful for detecting genetic diseases such  
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.  
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
CC involved in DNA amplification, replication, recombination or repair, the  
CC cancer is specifically associated with a gene selected from BRCA1 gene,  
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
CC method is also used for environmental monitoring, forensics and the food

```
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
CC
XX
SQ Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 other;
Query Match 78.6%; Score 11; DB 24; Length 20;
Best Local Similarity 91.7%; Pred. No. 5.2e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CACTGCACCTTNC 12
Db 16 CACTGCACCTTGC 5

RESULT 13
AB184974/c
ID AB184974 standard; DNA: 24 BP.
XX
AC AB184974:
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#1289 oligo #1.
XX
KW Human: K-ras: PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI: 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
```

```
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
CC
XX
SQ Sequence 24 BP; 6 A; 8 C; 7 G; 3 T; 0 other;
Query Match 78.6%; Score 11; DB 24; Length 24;
Best Local Similarity 91.7%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 CTGCACCTTNC 14
Db 22 CTGCACCTTGCCA 11

RESULT 14
AB184975
ID AB184975 standard; DNA: 24 BP.
XX
AC AB184975:
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#1289 oligo #2.
XX
KW Human: K-ras: PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI: 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
PT complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
```

CC and feed industry, detecting comprises scanning (using e.g. a scanning  
CC electron microscope and infrared microscope) the support at the  
CC particular sites and identifying if ligation of the oligonucleotide probe  
CC sets occurred and correlating (using a computer) identified ligation to a  
CC presence or absence of the target nucleotide sequences. AB192074 to  
CC AB197546 represent oligonucleotide sequences used in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 24 BP; 3 A; 7 C; 8 G; 6 T; 0 other;  
Query Match 78.6%; Score 11; DB 24; Length 24;  
Best Local Similarity 91.7%; Pred. No. 5.3e+03;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 CTGCACCTTNGCA 14  
|||||  
Db 3 CTGCACCTTGCCA 14  
RESULT 15  
AB190166/c  
ID AB190166 standard; DNA; 24 BP.  
XX  
AC AB190166;  
XX  
DT 15-FEB-2002 (first entry)  
XX  
DE Capture oligonucleotide zip ID#3885 oligo #1.  
XX  
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;  
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;  
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;  
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;  
KW environmental monitoring; food industry; feed industry; ss.  
XX  
OS Synthetic.  
XX  
PN WO200179548-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 04-APR-2001; 2001WO-US10958.  
XX  
PR 14-APR-2000; 2000US-197271P.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Barany F, Zivri M, Gerry NP, Favis R, Kliman R;  
XX  
DR WPI: 2002-034366/04.  
XX  
PT Designing capture oligonucleotide probes for use on a support to which  
XX complementary oligonucleotides hybridize with little mismatch -  
PS Example 5; Fig 25; 300pp; English.  
XX  
CC The present invention describes a method (M1) for designing capture  
CC oligonucleotide probes (I) for use on a support to which complementary  
CC oligonucleotide probes (II) will hybridize with little mismatch, where  
CC (i) have melting temperatures within a narrow range. The method is useful  
CC for detecting infectious diseases caused by bacterial infectious agents  
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal  
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and  
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,  
CC Epstein-Barr virus and polio virus, and parasitic infectious agents  
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus  
CC medialis. The method is also useful for detecting genetic diseases such  
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.  
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes  
CC involved in DNA amplification, replication, recombination or repair, the  
CC cancer is specifically associated with a gene selected from BRCA1 gene,  
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The  
CC method is also used for environmental monitoring, forensics and the food

CC and feed industry, detecting comprises scanning (using e.g. a scanning  
CC electron microscope and infrared microscope) the support at the  
CC particular sites and identifying if ligation of the oligonucleotide probe  
CC sets occurred and correlating (using a computer) identified ligation to a  
CC presence or absence of the target nucleotide sequences. AB192074 to  
CC AB197546 represent oligonucleotide sequences used in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;  
Query Match 78.6%; Score 11; DB 24; Length 24;  
Best Local Similarity 91.7%; Pred. No. 5.3e+03;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CACTGCACCTTNG 12  
|||||  
Db 16 CACTGCACCTTGC 5

Search completed: June 21, 2003, 22:26:25  
Job time : 79.7812 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 ; Search time 16.625 Seconds  
(without alignments)  
258.254 Million cell updates/sec

Title: US-09-964-666-12  
Perfect score: 14  
Sequence: 1 CACTGCACCTNCCA 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgn2\_6/ptodata1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata1/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13	92.9	25	2	US-08-713-557B-23
2	11.4	81.4	31	4	US-09-651-011A-29
3	11.4	81.4	20	4	US-09-246-277A-7
4	11.4	81.4	36	1	US-08-307-619-37
5	11.4	81.4	36	2	US-08-350-260A-83
6	11.4	81.4	36	2	US-08-350-260A-120
7	11.4	81.4	36	3	US-09-050-783-37
8	10.4	74.3	18	1	US-08-362-706A-2
9	10.4	74.3	18	4	US-09-549-808-2
C 10	10.4	74.3	20	4	US-09-021-701-469
C 11	10.4	74.3	20	4	US-09-021-701-470
C 12	10.4	74.3	20	4	US-09-021-701-471
C 13	10.4	74.3	20	4	US-09-021-701-472
C 14	10.4	74.3	20	4	US-09-021-701-473
C 15	10.4	74.3	20	4	US-09-021-701-474
C 16	10.4	74.3	20	4	US-09-021-701-475
C 17	10.4	74.3	20	4	US-09-021-701-476
C 18	10.4	74.3	20	4	US-09-484-617-148
C 19	10.4	74.3	21	1	US-08-289-187-2
C 20	10.4	74.3	21	4	US-09-495-797-31
C 21	10.4	74.3	21	5	PCT-US95-11114-2
C 22	10.4	74.3	22	2	US-09-056-691-4
C 23	10.4	74.3	22	3	US-08-812-515-4
C 24	10.4	74.3	27	4	US-09-418-720-23
C 25	10.4	74.3	36	1	US-09-384-327-15
C 26	10.4	74.3	36	1	US-08-458-372-15
C 27	10.4	74.3	36	6	5506118-6

28	10.4	74.3	41	1	US-08-307-619-61	Sequence 61, Appl
29	10.4	74.3	41	2	US-08-350-260A-107	Sequence 107, App
30	10.4	74.3	41	2	US-08-350-260A-208	Sequence 208, App
31	10.4	74.3	41	3	US-09-050-783-61	Sequence 61, Appl
32	10.4	74.3	44	2	US-08-350-260A-583	Sequence 583, App
C 33	10	71.4	20	1	US-08-564-002-1	Sequence 1, Appl
C 34	10	71.4	20	3	US-09-047-347-11	Sequence 11, Appl
C 35	10	71.4	20	4	US-09-517-584A-70	Sequence 70, Appl
C 36	10	71.4	20	4	US-09-180-437-231	Sequence 231, App
37	10	71.4	20	4	US-09-487-368A-177	Sequence 177, App
38	10	71.4	21	1	US-08-136-741-7	Sequence 7, Appl
C 39	10	71.4	22	4	US-09-460-145-6	Sequence 6, Appl
C 40	10	71.4	23	3	US-08-691-045-37	Sequence 37, Appl
C 41	10	71.4	30	4	US-09-000-094-1	Sequence 1, Appl
C 42	10	71.4	30	4	US-09-000-094-39	Sequence 39, Appl
C 43	10	71.4	33	4	US-08-169-715-47	Sequence 47, Appl
44	10	71.4	34	2	US-08-485-778-35	Sequence 35, Appl
45	10	71.4	34	3	US-08-520-550A-35	Sequence 35, Appl

## ALIGNMENTS

RESULT 1  
US-08-713-557B-23/C  
Sequence 23, Application US/08713557B  
Patent No. 5912168  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Rudert, Filiz  
TITLE OF INVENTION: CD95 REGULATORY GENE SEQUENCES  
TITLE OF INVENTION: AND TRANSCRIPTION FACTORS  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Law Offices of Ann W. Speckman  
STREET: 2601 Elliott Avenue, Suite 4185  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/713,557B  
FILING DATE: 30-AUG-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Speckman, Ann W  
REGISTRATION NUMBER: 31,881  
REFERENCE/DOCKET NUMBER: 11000.1004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565  
TELEFAX: 206-269-0563  
TELEX:  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: Linear  
US-08-713-557B-23  
Query Match 92.9% Score 13; DB 2; Length 25;  
Best Local Similarity 92.9%; Pred. No. 48;  
Matches 13; Conservative 0; Mismatches 1; Indels 0;  
Gaps 0;  
Oy 1 CACTGCACCTNCCA 14

Db 23 CACTGCATTTCACA 10

## RESULT 2

US-09-651-011A-29  
Sequence 29, Application US/09651011A  
Patent No. 6346416  
GENERAL INFORMATION:  
APPLICANT: Nicholas M. Dean  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF HPK/GCK-LIKE KINASE EXPRESSION  
FILE REFERENCE: RTS-0168  
CURRENT APPLICATION NUMBER: US/09/651,011A  
CURRENT FILING DATE: 2000-08-29  
NUMBER OF SEQ ID NOS: 49  
SEQ ID NO 29  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-651-011A-29

Query Match 81.4%; Score 11.4; DB 4; Length 20;  
Best Local Similarity 85.7%; Pred. No. 4e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACTGCATTTCACA 14  
Db 1 CACTGCATTTCACA 14

## RESULT 3

US-09-246-277A-7  
Sequence 7, Application US/09246277A  
Patent No. 6238866  
GENERAL INFORMATION:  
APPLICANT: Yeh, Homer R.; Wick, Charles H.  
TITLE OF INVENTION: NOVEL DETECTOR FOR NUCLEIC ACID  
TYPING AND METHODS OF USING THE SAME  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Office of the Chief Counsel  
STREET: U.S. Army SBCCOM  
CITY: APG(EA)  
STATE: Maryland  
COUNTRY: United States of America  
ZIP: 21010-3423.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/246,277A  
FILING DATE: 08-Feb-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Bifroni, U. John  
REGISTRATION NUMBER: 39908  
REFERENCE/DOCKET NUMBER: 436-96  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (410) 436-1158  
TELEFAX: (410) 436-2534  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO

ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: YNH24 Minisatellite  
SEQUENCE DESCRIPTION: SEQ ID NO: 7;  
US-09-246-277A-7

Query Match 81.4%; Score 11.4; DB 4; Length 31;  
Best Local Similarity 85.7%; Pred. No. 4.2e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACTGCATTTCACA 14  
Db 9 CACTGCATTTCACA 22

## RESULT 4

US-08-307-619-37  
Sequence 37, Application US/08307619  
Patent No. 5733743  
GENERAL INFORMATION:  
APPLICANT: Johnson, Kevin S  
APPLICANT: Winter, Gregory P  
APPLICANT: Griffiths, Andrew D  
APPLICANT: Smith, Andrew JH  
APPLICANT: Watchhouse, P  
TITLE OF INVENTION: Methods for producing members of specific  
NUMBER OF INVENTION: binding pairs  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/307,619  
FILING DATE: 16-SEP-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: G01N 33/531, G01N 33/68  
FILING DATE: 24-MAR-1993  
APPLICATION NUMBER: PCT/GB93/00605  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9206318.9  
FILING DATE: 24-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/00883  
FILING DATE: 15-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: David W. Clough  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 28111/32238  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-307-619-37

Query Match 81.4%; Score 11.4; DB 1; Length 36;  
Best Local Similarity 85.7%; Pred. No. 4.3e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



US-08-350-260A-120

Query Match 81.4%; Score 11.4; DB 2; Length 36;

Best Local Similarity 85.7%; Pred. No. 4.3e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14

DB 9 CAGTGCACCTTGCCA 22

RESULT 7

US-09-050-783-37

Sequence 37, Application US/09050783

Patent No. 6140471

GENERAL INFORMATION:

APPLICANT: Johnson, Kevin S

APPLICANT: Winter, Gregory P

APPLICANT: Griffiths, Andrew D

APPLICANT: Smith, Andrew JH

APPLICANT: Waterhouse, P

TITLE OF INVENTION: Methods for producing members of specific

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp; Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/050,783

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/307,619

FILING DATE: 16-SEP-1994

APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9206318.9

FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/00883

FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: David W. Clough

REGISTRATION NUMBER: 36,107

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-050-783-37

Query Match 81.4%; Score 11.4; DB 3; Length 36;

Best Local Similarity 85.7%; Pred. No. 4.3e+02;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14

DB 9 CAGTGCACCTTGCCA 22

RESULT 8

US-08-362-706A-2

Sequence 2, Application US/08362706A

Patent No. 5824794

GENERAL INFORMATION:

APPLICANT: Borden, Paula A.

APPLICANT: Heller, Renu A.

TITLE OF INVENTION: Human Stromelysin-1 Promoter

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Heller Ehrman White &amp; McCaulliffe

STREET: 525 University Avenue

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94301-1900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/362,706A

FILING DATE: 23-DEC-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Schmonsees, William

REGISTRATION NUMBER: 31796

REFERENCE/DOCKET NUMBER: 13265-1233

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 324-7000

TELEFAX: (650) 324-0638

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-362-706A-2

Query Match 74.3%; Score 10.4; DB 1; Length 18;

Best Local Similarity 84.6%; Pred. No. 1.5e+03;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCC 13

DB 3 CACTGCCCTTACC 15

RESULT 9

US-09-549-808-2

Sequence 2, Application US/09549808

Patent No. 6338944

GENERAL INFORMATION:

APPLICANT: Borden, Paula A.

APPLICANT: Heller, Renu A.

TITLE OF INVENTION: Human Stromelysin-1 Promoter

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Heller Ehrman White &amp; McCaulliffe

STREET: 525 University Avenue

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94301-1900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS



SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/549,808  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/174,756  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Schmonsees, William  
REGISTRATION NUMBER: 31796  
REFERENCE/DOCKET NUMBER: 13265-1233  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 324-7000  
TELEFAX: (650) 324-0638  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-549-808-2

Query Match 74.3% Score 10.4; DB 4; Length 18;  
Best Local Similarity 84.6%; Pred. No. 1.5e+03;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACCTNCC 13  
||||| ||| ||  
Db 3 CACTGCCCTTACC 15

RESULT 10  
US-09-021-701-469/C  
Sequence 469, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-8063  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 469:  
SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-021-701-469

Query Match 74.3% Score 10.4; DB 4; Length 20;  
Best Local Similarity 84.6%; Pred. No. 1.5e+03;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCACCTNCCA 14  
||||| ||| ||  
Db 20 ACTGCATTTACCA 8

## RESULT 11

US-09-021-701-470/C  
Sequence 470, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:

APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-8063  
TELEFAX: 650-236-2386  
INFORMATION FOR SEQ ID NO: 470:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-021-701-470

Query Match 74.3% Score 10.4; DB 4; Length 20;  
Best Local Similarity 84.6%; Pred. No. 1.5e+03;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCACCTNCCA 14  
||||| ||| ||  
Db 19 ACTGCATTTACCA 7

RESULT 12  
US-09-021-701-471/c  
Sequence 471, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 471:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-021-701-471

Query Match 74.3% Score 10.4; DB 4; Length 20;  
Best Local Similarity 84.6%; Pred. No. 1.5e+03;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCATTNCCA 14  
Db 18 ACTGCATTNCCA 6

RESULT 13  
US-09-021-701-472/c  
Sequence 472, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20  
STREET: 3000 Hanover Street

CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 472:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-09-021-701-472

Query Match 74.3% Score 10.4; DB 4; Length 20;  
Best Local Similarity 84.6%; Pred. No. 1.5e+03;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCATTNCCA 14  
Db 17 ACTGCATTNCCA 5

RESULT 14  
US-09-021-701-473/c  
Sequence 473, Application US/09021701  
Patent No. 6251588  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
APPLICANT: Wolber, Paul K.  
APPLICANT: Delenstarr, Glenda C.  
APPLICANT: Webb, Peter G.  
APPLICANT: Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/021,701  
FILING DATE: 10-FEB-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-236-2386  
 TELEFAX: 650-852-8063  
 INFORMATION FOR SEQ ID NO: 473:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-09-021-701-473

Query Match 74.3%; Score 10.4; DB 4; Length 20;  
 Best Local Similarity 84.6%; Pred. No. 1.5e+03;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCACTTNCCA 14  
 ||||| ||||  
 Db 16 ACTGCACTTACCA 4

RESULT 15  
 US-09-021-701-474/C  
 Sequence 474, Application US/09021701  
 Patent No. 6251588  
 GENERAL INFORMATION:  
 APPLICANT: Shannon, Karen W.  
 APPLICANT: Wolfer, Paul K.  
 APPLICANT: Delenstarr, Glenda C.  
 APPLICANT: Webb, Peter G.  
 APPLICANT: Kincaid, Robert H.  
 TITLE OF INVENTION: Methods for evaluating oligonucleotide  
 NUMBER OF SEQUENCES: 1165  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20  
 STREET: 3000 Hanover Street  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/021,701  
 FILING DATE: 10-FEB-1998  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Choi, Wendy A.  
 REGISTRATION NUMBER: 36,697  
 REFERENCE/DOCKET NUMBER: 10971464-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-236-2386  
 TELEFAX: 650-852-8063  
 INFORMATION FOR SEQ ID NO: 474:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 20 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-09-021-701-474

Query Match 74.3%; Score 10.4; DB 4; Length 20;  
 Best Local Similarity 84.6%; Pred. No. 1.5e+03;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCACTTNCCA 14  
 ||||| ||||  
 Db 15 ACTGCACTTACCA 3

Search completed: June 22, 2003, 00:01:34  
 Job time: 18.625 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compen Gen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 22:26:37 ; Search time 41.3438 Seconds  
(without alignments)  
496.907 Million cell updates/sec

Title: US-09-964-666-12  
Perfect score: 14  
Sequence: 1 CACTGCACCTNCCA 14

Scoring table: IDENTITY\_NUC  
Gap 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_NA.\*  
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2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	92.9	14	9	US-09-964-667-12
2	13	92.9	14	10	US-09-964-666-12
3	13	92.9	14	10	US-09-964-412-12
4	11.4	81.4	20	9	US-10-105-004-97
5	11.4	81.4	25	9	US-10-215-112-2203
6	11.4	81.4	25	9	US-10-098-263B-65254
7	10.4	74.3	20	9	US-09-784-674-469
8	10.4	74.3	20	9	US-09-784-674-470
9	10.4	74.3	20	9	US-09-784-674-471
10	10.4	74.3	20	9	US-09-784-674-472
11	10.4	74.3	20	9	US-09-784-674-473
12	10.4	74.3	20	9	US-09-784-674-474
13	10.4	74.3	20	9	US-09-784-674-475
14	10.4	74.3	20	9	US-09-784-674-476
15	10.4	74.3	20	9	US-09-887-145-27
16	10.4	74.3	20	9	US-10-181-107-148
17	10.4	74.3	22	9	US-09-996-956-14
18	10.4	74.3	25	9	US-10-215-112-4856
19	10.4	74.3	25	9	US-10-098-263B-30929

20	10.4	74.3	25	9	US-10-098-263B-48658	Sequence 48658, A
21	10.4	74.3	25	9	US-10-098-263B-53671	Sequence 53671, A
22	10.4	74.3	25	9	US-10-098-263B-94806	Sequence 94806, A
23	10.4	74.3	25	9	US-10-098-263B-121462	Sequence 121462, A
24	10.4	74.3	26	9	US-10-121-857-80	Sequence 80, Appl
25	10.4	74.3	30	9	US-10-113-794A-3	Sequence 3, Appl1
26	10.4	74.3	44	10	US-09-988-899-65	Sequence 65, Appl
27	10.4	74.3	45	9	US-09-905-291A-275	Sequence 275, Appl
28	10.4	74.3	45	9	US-09-902-853-275	Sequence 275, Appl
29	10.4	74.3	45	9	US-09-907-824-275	Sequence 275, Appl
30	10.4	74.3	45	9	US-09-907-841-275	Sequence 275, Appl
31	10.4	74.3	45	9	US-09-904-011-275	Sequence 275, Appl
32	10.4	74.3	45	9	US-09-906-742-275	Sequence 275, Appl
33	10.4	74.3	45	9	US-09-906-838-275	Sequence 275, Appl
34	10.4	74.3	45	9	US-09-907-613-275	Sequence 275, Appl
35	10.4	74.3	45	9	US-09-907-942-275	Sequence 275, Appl
36	10.4	74.3	45	9	US-09-904-820-275	Sequence 275, Appl
37	10.4	74.3	45	9	US-09-904-859-275	Sequence 275, Appl
38	10.4	74.3	45	9	US-09-904-820-275	Sequence 275, Appl
39	10.4	74.3	45	9	US-09-904-786-275	Sequence 275, Appl
40	10.4	74.3	45	9	US-09-906-646-275	Sequence 275, Appl
41	10.4	74.3	45	9	US-09-906-700-275	Sequence 275, Appl
42	10.4	74.3	45	9	US-09-902-903-275	Sequence 275, Appl
43	10.4	74.3	45	9	US-09-903-749A-275	Sequence 275, Appl
44	10.4	74.3	45	9	US-09-903-786-275	Sequence 275, Appl
45	10.4	74.3	45	9	US-09-902-736-275	Sequence 275, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-964-667-12  
Sequence 12, Application US/09964667  
Publication No. US20030033621A1

GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment of Preventio  
Of Alzheimer's Disease

NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., Suite 600  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20005-3934

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,667  
FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-964-667-12

Query Match 92.9%; Score 13; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14  
DB 1 CACTGCACCTTNCCA 14

RESULT 2

US-09-964-666-12  
Sequence 12, Application US/09964666  
Patent No. US20020104108A1  
GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Steine, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-964-666-12

Query Match 92.9%; Score 13; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14  
DB 1 CACTGCACCTTNCCA 14

RESULT 3

US-09-964-412-12  
Sequence 12, Application US/09964412  
Patent No. US20020129391A1  
GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Steine, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Query Match 92.9%; Score 13; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14  
DB 1 CACTGCACCTTNCCA 14

RESULT 4

US-10-105-004-97/C  
Sequence 97, Application US/10105004  
Publication No. US20030105002A1  
GENERAL INFORMATION:

APPLICANT: Murray, Jeffrey

TITLE OF INVENTION: RIES COMPOSITIONS AND THERAPEUTIC  
AND DIAGNOSTIC USES THEREFOR

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG &amp; ELLIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/105,004

FILING DATE: 22-Mar-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/754,477

FILING DATE: 22-Nov-1996

ATTORNEY/AGENT INFORMATION:

```
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-022.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-105-004-97

Query Match
Best Local Similarity 81.4%; Score 11.4; DB 9; Length 20;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14
    ||||| |||
Db 20 CACTGCACCTCCCA 7

RESULT 5
US-10-215-112-2203
Sequence 2203, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Miltman
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2203
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2203

Query Match
Best Local Similarity 81.4%; Score 11.4; DB 9; Length 25;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14
    ||||| |||
Db 4 CACGGCATTTCGA 17

RESULT 6
US-10-098-263B-65254
Sequence 65254, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 65254
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
```

```
US-10-098-263B-65254

Query Match
Best Local Similarity 81.4%; Score 11.4; DB 9; Length 25;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14
    ||||| |||
Db 8 CACTGCATTACCA 21

RESULT 7
US-09-784-674-469/C
Sequence 469, Application US/09784674
Publication No. US20030054346A1
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
Wolber, Paul K.
Delenstarr, Glenda C.
Webb, Peter G.
Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
probe sequences
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
Company M/S 2080
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,674
FILING DATE: 15-Feb-2001
CLASSIFICATION: No. US20030054346A1 available
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/021,701
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 469:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 469:
US-09-784-674-469

Query Match
Best Local Similarity 74.3%; Score 10.4; DB 9; Length 20;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCATTNCCA 14
    ||||| |||
Db 20 ACTGCATTACCA 8

RESULT 8
```

US-09-784-674-470/c  
; Sequence 470, Application US/09784674  
; Publication No. US20030054346A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Karen W.  
; Wolber, Paul K.  
; Delenstarr, Glenda C.  
; Webb, Peter G.  
; Kincaid, Robert H.  
; TITLE OF INVENTION: Methods for evaluating oligonucleotide  
; probe sequences  
; NUMBER OF SEQUENCES: 1165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard  
; Company M/S 2080  
; STREET: 3000 Hanover Street  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/784,674  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: No. US20030054346A1 available  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/021,701  
; FILING DATE: 10-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Choi, Wendy A.  
; REGISTRATION NUMBER: 36,697  
; REFERENCE/DOCKET NUMBER: 10971464-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-8063  
; TELEFAX: 650-852-8063  
; INFORMATION FOR SEQ ID NO: 470:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 470:  
US-09-784-674-470  
Query Match 74.3%; Score 10.4; DB 9; Length 20;  
Best Local Similarity 84.6%; Pred. No. 1e+04; 2; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 2 ACTGCACCTTACCA 14  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 ACTGCATTACCA 7  
RESULT 9  
US-09-784-674-471/c  
; Sequence 471, Application US/09784674  
; Publication No. US20030054346A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Karen W.  
; Wolber, Paul K.  
; Delenstarr, Glenda C.  
; Webb, Peter G.  
; Kincaid, Robert H.  
; TITLE OF INVENTION: Methods for evaluating oligonucleotide  
; probe sequences  
; NUMBER OF SEQUENCES: 1165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard  
; COMPANY M/S 2080  
; STREET: 3000 Hanover Street  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/784,674  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: No. US20030054346A1 available  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/021,701  
; FILING DATE: 10-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Choi, Wendy A.  
; REGISTRATION NUMBER: 36,697  
; REFERENCE/DOCKET NUMBER: 10971464-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-852-8063  
; TELEFAX: 650-852-8063  
; INFORMATION FOR SEQ ID NO: 471:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 471:  
US-09-784-674-471

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard  
Company M/S 2080  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/784,674  
FILING DATE: 15-Feb-2001  
CLASSIFICATION: No. US20030054346A1 available  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/021,701  
FILING DATE: 10-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-8063  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 471:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 471:  
US-09-784-674-471  
Query Match 74.3%; Score 10.4; DB 9; Length 20;  
Best Local Similarity 84.6%; Pred. No. 1e+04; 2; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 2 ACTGCACCTTACCA 14  
| | | | | | | | | | | | | | | | | | | | | |  
Db 18 ACTGCATTACCA 6  
RESULT 10  
US-09-784-674-472/c  
; Sequence 472, Application US/09784674  
; Publication No. US20030054346A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Karen W.  
; Wolber, Paul K.  
; Delenstarr, Glenda C.  
; Webb, Peter G.  
; Kincaid, Robert H.  
; TITLE OF INVENTION: Methods for evaluating oligonucleotide  
; probe sequences  
; NUMBER OF SEQUENCES: 1165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard  
; COMPANY M/S 2080  
; STREET: 3000 Hanover Street  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS



SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/784,674  
FILING DATE: 15-Feb-2001  
CLASSIFICATION: No. US20030054346A1 available  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/021,701  
FILING DATE: 10-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-8063  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 472:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 472:  
US-09-784-674-472

Query Match  
Best Local Similarity 74.3%; Score 10.4; DB 9; Length 20;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14  
Db 17 ACTGCATTACCA 5

RESULT 11  
US-09-784-674-473/c  
Sequence 473, Application US/09784674  
Publication No. US20030054346A1  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
Wolber, Paul K.  
DeJenstarr, Glenda C.  
Webb, Peter G.  
Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard  
Company M/S 20B0  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/784,674  
FILING DATE: 15-Feb-2001  
CLASSIFICATION: No. US20030054346A1 available  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/021,701  
FILING DATE: 10-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-236-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 473:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 473:  
US-09-784-674-473

Query Match  
Best Local Similarity 74.3%; Score 10.4; DB 9; Length 20;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14  
Db 16 ACTGCATTACCA 4

RESULT 12  
US-09-784-674-474/c  
Sequence 474, Application US/09784674  
Publication No. US20030054346A1  
GENERAL INFORMATION:  
APPLICANT: Shannon, Karen W.  
Wolber, Paul K.  
DeJenstarr, Glenda C.  
Webb, Peter G.  
Kincaid, Robert H.  
TITLE OF INVENTION: Methods for evaluating oligonucleotide  
NUMBER OF SEQUENCES: 1165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard  
Company M/S 20B0  
STREET: 3000 Hanover Street  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/784,674  
FILING DATE: 15-Feb-2001  
CLASSIFICATION: No. US20030054346A1 available  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/021,701  
FILING DATE: 10-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Choi, Wendy A.  
REGISTRATION NUMBER: 36,697  
REFERENCE/DOCKET NUMBER: 10971464-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-236-2386  
TELEFAX: 650-852-8063  
INFORMATION FOR SEQ ID NO: 474:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 474:  
US-09-784-674-474

Query Match 74.3%; Score 10.4; DB 9; Length 20;  
Best Local Similarity 84.6%; Pred. No. 1e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14  
||||| |||||  
DB 15 ACTGCATTACCA 3

RESULT 13

US-09-784-674-475/c  
Sequence 475, Application US/09784674  
Publication No. US20030054346A1

GENERAL INFORMATION:

APPLICANT: Shannon, Karen W.

Wolber, Paul K.

Delenstarr, Glenda C.

Webb, Peter G.

Kincaid, Robert H.

TITLE OF INVENTION: Methods for evaluating oligonucleotide  
probe sequences

NUMBER OF SEQUENCES: 1165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard

STREET: 3000 Hanover Street

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/784, 674

FILING DATE: 15-Feb-2001

CLASSIFICATION: No. US20030054346A1 available

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/021,701

FILING DATE: 10-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Choi, Wendy A.

REGISTRATION NUMBER: 36,697

REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 475:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 475:

US-09-784-674-475

Query Match 74.3%; Score 10.4; DB 9; Length 20;  
Best Local Similarity 84.6%; Pred. No. 1e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14  
||||| |||||  
DB 14 ACTGCATTACCA 2

RESULT 14

US-09-784-674-476/c  
Sequence 476, Application US/09784674  
Publication No. US20030054346A1

GENERAL INFORMATION:

APPLICANT: Shannon, Karen W.

Wolber, Paul K.

Delenstarr, Glenda C.

Webb, Peter G.

Kincaid, Robert H.

TITLE OF INVENTION: Methods for evaluating oligonucleotide  
probe sequences

NUMBER OF SEQUENCES: 1165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard

STREET: 3000 Hanover Street

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/784, 674

FILING DATE: 15-Feb-2001

CLASSIFICATION: No. US20030054346A1 available

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/021,701

FILING DATE: 10-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Choi, Wendy A.

REGISTRATION NUMBER: 36,697

REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 476:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 476:

US-09-784-674-476

Query Match 74.3%; Score 10.4; DB 9; Length 20;  
Best Local Similarity 84.6%; Pred. No. 1e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14  
||||| |||||  
DB 13 ACTGCATTACCA 1

RESULT 15

US-09-887-145-27  
Sequence 27, Application US/09887145  
Publication No. US20030082139A1

GENERAL INFORMATION:

APPLICANT: Kim, Seung U

TITLE OF INVENTION: Immortalized human microglia  
cell and continuous cell line

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: David Prashker, Esq.

STREET: P.O. Box 5387

CITY: Magnolia  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 01930  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
COMPUTER: Dell PC  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Microsoft word version 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/887,145  
FILING DATE: 22-Jun-2001  
CLASSIFICATION: Unknown  
ATTORNEY/AGENT INFORMATION:  
NAME: David Prashker, Esq.  
REGISTRATION NUMBER: 29,693  
REFERENCE/DOCKET NUMBER: UBC-002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (978) 525-3794  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-887-145-27

Query Match 74.3%; Score 10.4; DB 9; Length 20;  
Best Local Similarity 84.6%; Pred. No. 1e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14  
Db 7 ACTGCACCTGGCCA 19

Search completed: June 22, 2003, 03:18:21  
Job time : 43.3438 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:28:37 ; Search time 604.724 Seconds  
(without alignments)  
374.936 Million cell updates/sec

Title: US-09-964-666-12  
Perfect score: 14  
Sequence: 1 CACTGCACCTNCCA 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estipl:\*  
7: em\_estiro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12	85.7	50	9	AU105465
C 2	11	78.6	36	13	AU105465 AU105465
C 3	11	78.6	39	17	AU105465 AU105465
C 4	11	78.6	44	10	AU105465 AU105465
C 5	10.4	74.3	22	17	AU105465 AU105465
C 6	10.4	74.3	29	17	AU105465 AU105465

Result No.	Score	Query Match	Length	DB ID	Description
C 7	10.4	74.3	41	17	AU105465 AU105465
C 8	10.4	74.3	50	9	AU105465 AU105465
C 9	10	71.4	34	17	AU105465 AU105465
C 10	10	71.4	46	17	AU105465 AU105465
C 11	10	71.4	47	17	AU105465 AU105465
C 12	10	71.4	48	13	AU105465 AU105465
C 13	10	71.4	49	14	AU105465 AU105465
C 14	9.8	70.0	25	17	AU105465 AU105465
C 15	9.8	70.0	26	17	AU105465 AU105465
C 16	9.8	70.0	28	9	AU105465 AU105465
C 17	9.8	70.0	30	17	AU105465 AU105465
C 18	9.8	70.0	31	17	AU105465 AU105465
C 19	9.8	70.0	32	17	AU105465 AU105465
C 20	9.8	70.0	34	17	AU105465 AU105465
C 21	9.8	70.0	36	17	AU105465 AU105465
C 22	9.8	70.0	37	17	AU105465 AU105465
C 23	9.8	70.0	38	17	AU105465 AU105465
C 24	9.8	70.0	40	9	AU105465 AU105465
C 25	9.8	70.0	41	17	AU105465 AU105465
C 26	9.8	70.0	42	17	AU105465 AU105465
C 27	9.8	70.0	43	17	AU105465 AU105465
C 28	9.8	70.0	46	9	AU105465 AU105465
C 29	9.8	70.0	46	14	AU105465 AU105465
C 30	9.8	70.0	47	17	AU105465 AU105465
C 31	9.8	70.0	47	17	AU105465 AU105465
C 32	9.8	70.0	49	17	AU105465 AU105465
C 33	9.8	70.0	50	9	AU105465 AU105465
C 34	9.8	70.0	50	9	AU105465 AU105465
C 35	9.8	70.0	50	9	AU105465 AU105465
C 36	9.4	67.1	27	17	AU105465 AU105465
C 37	9.4	67.1	29	17	AU105465 AU105465
C 38	9.4	67.1	31	17	AU105465 AU105465
C 39	9.4	67.1	35	9	AU105465 AU105465
C 40	9.4	67.1	36	12	AU105465 AU105465
C 41	9.4	67.1	38	17	AU105465 AU105465
C 42	9.4	67.1	41	17	AU105465 AU105465
C 43	9.4	67.1	42	17	AU105465 AU105465
C 44	9.4	67.1	43	9	AU105465 AU105465
C 45	9.4	67.1	43	9	AU105465 AU105465

## ALIGNMENTS

RESULT 1  
LOCUS AU105465/50 bp mRNA linear EST 30-AUG-2001  
DEFINITION AU105465 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
ACCESSION HRC09846, mRNA sequence.  
VERSION AU105465  
KEYWORDS AU105465.1 GI:13554986  
SOURCE EST.  
ORGANISM human.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Suzuki,T., Taira,H., Tsunoda,T., Mizushima,Sugano,J., Sese,J., Hata  
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
JOURNAL MEDLINE  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki,T., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
,S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 145-156 (1997).  
FEATURES Location/Qualifiers

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source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC09846"
/clone_1lb="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated u937 cells"
BASE COUNT      12 a      12 c      14 g      12 t
ORIGIN

Query Match      85.7%;   Score 12;   DB 9;   Length 50;
Best Local Similarity 92.3%;   Pred. No. 2.2e+04;
Matches 12;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      1 CACTGCACCTTNC 13
        ||||||
        32 CACTGCACCTTACC 20

RESULT 2
BJ066024
LOCUS
DEFINITION
Bj066024 NIBB Mochii normalized xenopus tailbud library Xenopus
laevis cDNA clone XL084015 5', mRNA sequence.
ACCESSION
BJ066024
VERSION
BJ066024.1 GI:17479075
KEYWORDS
EST.
SOURCE
African clawed frog.
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea;
Xenopodidae; Xenopus.
1 (bases 1 to 36)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
,Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1..36
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL084015"
/clone_1lb="NIBB Mochii normalized Xenopus tailbud
library"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; CDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC institute)."
BASE COUNT      12 a      6 c      8 g      10 t
ORIGIN

Query Match      78.6%;   Score 11;   DB 13;   Length 36;
Best Local Similarity 91.7%;   Pred. No. 6.9e+04;
Matches 11;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2 ACTGCACCTTNC 13
        ||||||
        13 ACTGCACCTTACC 24

RESULT 3
A2936711
LOCUS
39 bp      DNA      linear      GSS 26-APR-2001
A2936711

```

DEFINITION	2M0193103R Mouse 10kb plasmid UNGC2M library Mus musculus genomic			
ACCESSION	A2936711.1 GI:13795292			
VERSION	GSS.			
KEYWORDS	house mouse;			
SOURCE	Mus musculus.			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.			
AUTHORS	1 (bases 1 to 39) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0193 row: 1 column: 03 Seq primer: CACACAGCAACACACTATGACC Class: plasmid ends High quality sequence stop: 39. location/Qualifiers 1..39 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UNG2M0193103" /clone_lib="Mouse 10kb plasmid UNGC2M library" /sex="Female" /lab_host="E. coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[gb AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
BASE COUNT	10 a 10 c 8 g 11 t			
ORIGIN				
Query Match	78.6%; Score 11; DB 17; Length 39;			
Best Local Similarity	91.7%; Pred. No. 7e+04;			
Matches 11; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
Oy	2 ACTGCACCTTNC 13 			
Db	15 ACTGCACCTTCC 26			
RESULT 4	44 bp mRNA linear EST 14-MAR-2002			
LOCUS	AN962509			

DEFINITION	AV962509 Nori Satoh unpublished cDNA library, larva Clona intestinalis cDNA clone c11v13117 5', mRNA sequence.
ACCESSION	AV962509
VERSION	AV962509.1
KEYWORDS	GI:19450808
SOURCE	EST.
ORGANISM	Clona intestinalis. Clona intestinalis Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona Phlebobranchia; Cloniidae; Clona. 1 (bases 1 to 44) Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T. Expressed genes in Clona intestinalis Unpublished (2000) Contact: Nori Satoh Department of Zoology Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-4081 Fax: 81-75-705-1113 Email: satoh@ascidian.zool.kyoto-u.ac.jp. location/Qualifiers 1..44 /organism="Clona intestinalis" /db_xref="taxon:7719" /clone="c11v13117" /clone_lib="Nori Satoh unpublished cDNA library, larva" /tissue_type="whole animal" /dev_stage="larva" /note="Vector: pBluescript SK"
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
BASE COUNT	9 a 9 c 11 g 15 t
ORIGIN	

Query Match	78.6%	Score 11	DB 10	Length 44
Best Local Similarity	91.7%	Pred. No. 7	2e+04	
Matches	11	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0
QY	2	ACTGCACCTTNC	13	
Db	2	ACTGCACCTTGC	13	

RESULT 5	22 bp	DNA	linear	GSS 29-SEP-2000
AZ309394/c				
LOCUS				
DEFINITION	IM0013P222	Mouse 10kb plasmid	U00C1M library	Mus musculus genomic
ACCESSION	AZ309394			
VERSION	AZ309394.1	GI:10350335		
KEYWORDS	GSS.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
	1 (bases 1 to 22)			
	Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamil,C.,			
	Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly			
	,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.			
	and Wright,D., Weiss,R.			
	Mouse whole genome scaffolding with paired end reads from 10kb			
	plasmid inserts			
	unpublished (2000)			
JOURNAL	Contact: Robert B. Weiss			
COMMENT	University of Utah Genome Center			
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT			
	84112, USA			
	Tel: 801 585 5606			
	Fax: 801 585 7177			
	Email: dunn@genetics.utah.edu			
	Insert length: 10000 Std Error: 0.00			
	Plate: 0013 row: P column: 22			
	Seq primer: CACACAGGAAACACGTATGACC			
	Class: plasmid ends			

```

FEATURES
SOURCE

High quality sequence stop: 22.
location/qualifiers
1. 22
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M001.3p22"
/clone_lib="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F- "
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (91473211419bAfr129072.1), a copy-number
inducible derivative of pAfr129072.1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

	Query Match	Similarity	Score 10.4	DB 17	Length 22
db	Best Local	84.6%	Pred. No. 1.3e+05		
	Matches 11	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	1 CACTGCACTTNCG	13			
	11				
	14 CAAATGCACTTCCC	2			

	RESULT 6			
AZ801886/c	LOCUS	AZ801886	29 bp	DNA linear GSS 16-FEB-2001
	DEFINITION	2K006G0103X Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0060103 R, DNA sequence.		
	ACCESSION	AZ801886		
	VERSION	AZ801886.1	GI:12954209	
	KEYWORDS	GSS.		
SOURCE	ORGANISM	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 29) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Petersen,T., Reilly, 'M., Rose,M., Rogse,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10xb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0060 Row: I Column: 03 Seq primer: CACACAGCAAAACACTTGACC Class: plasmid ends		





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/clone="CAS05488"
/clone_lib="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylfumarate treated u937 cells"
BASE COUNT
19 a 7 c 16 g 8 t
ORIGIN

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Query Match	74.3%	Score 10.4	DB 9	Length 50
Best Local Similarity	84.6%	Pred. No. 1.5e+05		
Matches 11	Conservative	0	Mismatches 2	Indels 0
				Gaps 0
Q7	1 CACTGCACCTTNC	13		
Db	34 CACTGCCCTTACC	22		

RESULT	9
A2470763/c	
LOCUS	34 bp DNA linear GSS 04-OCT-2000
DEFINITION	IM0285F10F Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C1M0285F10 F, DNA sequence.
DESCRIPTION	U06C1M0285F10F

SOURCE ORGANISM	house mouse. Mus musculus
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4	4
5	5
6	6
7	7
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100	100

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamill, C.,  
1 (Pages 1 to 34)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
**JOURNAL** Plasmid inserts  
**COMMENT** Unpublished (2000) Weis  
Contact: Robert B.  
University of Utah  
Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT  
84112-0002

041126058  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0285 row: F column: 10  
Seq primer: CGTGTAAACGACGCCACAT  
Class: plasmid ends  
High quality sequence stop: 34.

FEATURES	Location/Qualifiers
source	1. .34

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0285F10"
/clone_lib="Mouse 10kb plasmid UUCGM library"
/sex="Male"

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"/  
/note="Vector: pWD42n"; Purified genomic DNA from *M. musculus* C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.max.org/resources/documents/dnafrag/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

Inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	71.4%	Score 10:	DB 17:	Length 34:
Best Local Similarity	90.9%	Pred No. 2.2e+05:		
Matches	10:	Conservative	0:	Mismatches 1:
				Indels 0:
				Gaps 0:
QY	4	TGCACTTNCCA	14	
db	13	TGCACTTCCCA	3	

RESULT 10	LOCUS	DEFINITION
AL772108/c	46 bp	DNA linear GSS 19-JUN-2002
AL772108		Arbidopsis thaliana T-DNA flanking sequence GK-186B11-014622,, genomic survey sequence.

NETWORKS	655.
SOURCE	thale cress.
ORGANISM	Arabidopsis

**REFERENCE**

1. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
2  
unpublished  
(flanking sequence tags) from Arabidopsis thaliana T-DNA  
transformed lines  
Rosso, M., Strilchov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.  
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
for flanking sequence tag based reverse genetics

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	COMMENT
unpublished 3 (bases 1 to 46) L.I., Y. Strelizhov, N., Rosso, M. and Weissnaar, B. Direct Submission Submitted (17-JUN-2002) Weissnaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50825, Germany This sequence is recovered from the left border of the r-DNA. It indicates an insertion close to or within gene At2g48150. The sequences are generated at the MPI for Plant Breeding Research in	

the context of the GABI-Kat project. GABI-Kat is a large-scale Arabidopsis thaliana Plant Genomics program designated 'GABI-Kat'.

```
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-kat/.
location/Qualifiers
1. .46
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
```

```

/db_xref="taxon:3702"
/clone="GR-186B11-014622"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana

```

plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the *A. thaliana* nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT	15 a	6 c	8 g	17 t
ORIGIN				
Query Match	71.4%; Score 10; DB 17; Length 46			

Best Local Similarity 90.9%; Pred. No. 2.4e+05;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGCACCTNCCA 14  
1111111111  
DB 21 TGCACCTTACCA 11

## RESULT 11

AZ462142/c

LOCUS 47 bp DNA linear GSS 04-OCT-2000  
DEFINITION IM0269K14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0269K14 F, DNA sequence.

ACCESSION

AZ462142

VERSION

AZ462142.1

KEYWORDS

GSS.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

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COMMENT

Best Local Similarity 100.0%; Pred. No. 2.4e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGCACCTT 10  
1111111111  
DB 34 CACTGCACCTT 25

## RESULT 12

BJ034300

LOCUS 48 bp mRNA linear EST 06-DEC-2001  
DEFINITION BJ034300 NIBB Mochil normalized Xenopus neurula library Xenopus  
laevis cDNA clone XL028b09 5', mRNA sequence.

ACCESSION

BJ034300

VERSION

BJ034300.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

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Best Local Similarity 90.9%; Pred. No. 2.4e+05;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CTGCACCTNCC 13  
1111111111  
DB 16 CTGCACCTTACC 26

## RESULT 13

C20876

LOCUS 49 bp mRNA linear EST 23-OCT-1996  
DEFINITION HMG50004943 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA  
sequence.

ACCESSION

C20876

VERSION

C20876.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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**TITLE** BodyMap: human gene expression database  
**JOURNAL** Unpublished (1995)  
**COMMENT** Contact: Okubo, K.  
 Institute for Molecular and Cellular Biol  
 Osaka University  
 1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan  
 Tel: 06-877-5111(ex.3315)  
 Email: kousakujimb.osaka-u.ac.jp  
 Human Gene Signature, 3'-directed CDNA sequence. We are not  
 submitting the same CDNA sequence redundantly to DBJ since 1993.  
 For the abundance information of clones with this sequence in this  
 library and as well as in other 3'-directed libraries, see  
 http://www.imcb.osaka-u.ac.jp/bodymap/. The sequences of the clones  
 represented by this GS sequence is also found there.

**FEATURES**  
**source**  
 1.49  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Human adult (K.Okubo)"  
 /dev\_stage="adult"  
 /note="Organ: blood; Vector: l-gt-11; Site: 1; Eco-RI;  
 Monocytes were prepared from blood by ficoll-hypaque,  
 percoll and T cell rosetting purification steps (purity:  
 96 %). mRNA was prepared from activated monocytes from a  
 patient with rheumatoid arthritis. mRNA was reverse  
 transcribed with MLV. Using Eco-RI linkers CDNA was  
 cloned into l-gt-11 vector arms. The CDNA library was  
 screened by differential hybridization using radioactively  
 marked ss-cDNA from activated and non-activated  
 monocytes."

**BASE COUNT**  
 ORIGIN  
 10 a 17 c 12 g 9 t 1 others

**Query Match** 71.4%; Score 10; DB 14; Length 49;  
**Best Local Similarity** 83.3%; Pred. No. 2.4e+05;  
**Matches** 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 1 CACTGCACCTTNC 12  
 11111111 1  
**Db** 9 CACTGCACCTNCC 20

**RESULT 14**  
**AZ481615** 25 bp DNA linear GSS 04-OCT-2000  
**LOCUS** 1M0306A03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
**DEFINITION** clone UUGC1M0306A03 F, DNA sequence.  
**ACCESSION** AZ481615  
**VERSION** AZ481615.1 GI:10642680  
**KEYWORDS** GSS.  
**SOURCE** house mouse.  
**ORGANISM** Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE**  
**AUTHORS** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Dival, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.  
 and Wright, D., Weiss, R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0306 row: A column: 03  
 Seq primer: CGTTGTAACGACGCGCAGT

**FEATURES**  
**source**  
 1.25  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0306A03"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: pMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g114732114|p1AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptor complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

**BASE COUNT**  
 ORIGIN  
 8 a 6 c 6 g 5 t

**Query Match** 70.0%; Score 9.8; DB 17; Length 25;  
**Best Local Similarity** 78.6%; Pred. No. 2.7e+05;  
**Matches** 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**QY** 1 CACTGCACCTTNC 14  
 11111111 11  
**Db** 5 CGCTGCACCTTACA 18

**RESULT 15**  
**HSTEA0309** 26 bp mRNA linear GSS 30-JAN-1996  
**LOCUS** HSTEA0309  
**DEFINITION** H.sapiens trapped exon SNSA0309, genomic survey sequence.  
**ACCESSION** X85346  
**VERSION** X85346.1 GI:1008100  
**KEYWORDS** GSS; chromosome 21.  
**SOURCE** Homo sapiens.  
**ORGANISM** Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
**REFERENCE**  
**AUTHORS** Lucante, D., Chen, H.M., Shea, D., Sane, S.N., Rutter, M., Chras, R.,  
 Rossier, C., Buckler, A., Antonarakis, S.E. and McCormick, M.R.  
**TITLE** Localization of 102 exons to a 2.5 Mb region involved in Down  
 syndrome  
**JOURNAL** Hum. Mol. Genet. 4 (8), 1305-1311 (1995)  
**COMMENT** MEDLINE 96090248  
 PUBMED 7581367  
**REFERENCE** 2 (bases 1 to 26)  
**AUTHORS** Antonarakis, S.E.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (14-MAR-1995) S.E. Antonarakis, Div. of Medical Genetics,  
 Univ. and Cantonal Hospital of Geneva, CMU, 1 Rue Michel-Servet,  
 CH- 1211 Geneva, SWITZERLAND  
**FEATURES**  
**source**  
 1.26  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="21"  
 /map="21q22.2-22.3"

BASE COUNT 2 a /note="trapped exon sequence"  
ORIGIN 11 c 4 g 9 t

Query Match 70.0%; Score 9.8; DB 17; Length 26;  
Best Local Similarity 78.6%; Pred. No. 2.7e+05;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CACTGCACCTTNCCA 14  
1 |||||  
DB 12 CCCTGCACCTGTCCA 25

Search completed: June 21, 2003, 23:59:01  
Job time : 610.901 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 281.094 Seconds

(without alignments)  
1449.478 Million cell updates/sec

Title: US-09-964-666-13

Perfect score: 14

Sequence: 1 CCAGGTGTAGNCCA 14

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rtd:\*

36: em\_htg\_mam:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11.4	81.4	50	6 AX190063	AX190063 Sequence
2	11.4	81.4	50	6 AX190065	AX190065 Sequence
3	11	78.6	15	6 AR179980	AR179980 Sequence
4	11	78.6	31	6 AX249591	AX249591 Sequence
5	10.4	74.3	15	6 AR132395	AR132395 Sequence
6	10.4	74.3	15	6 AR132396	AR132396 Sequence
7	10.4	74.3	18	12 AB067924	AB067924 Synthetic
8	10.4	74.3	19	6 AX027079	AX027079 Sequence
9	10.4	74.3	20	4 BOVDIK06	BOVDIK06 Sequence
10	10.4	74.3	20	6 AR099541	AR099541 Sequence
11	10.4	74.3	20	6 AR146442	AR146442 Sequence
12	10.4	74.3	20	6 AR178822	AR178822 Sequence
13	10.4	74.3	20	6 AX298604	AX298604 Sequence
14	10.4	74.3	20	12 AB068080	AB068080 Synthetic
15	10.4	74.3	22	6 AX180631	AX180631 Sequence
16	10.4	74.3	24	6 A47937	A47937 Sequence
17	10.4	74.3	24	6 AR090957	AR090957 Sequence
18	10.4	74.3	24	6 AR176982	AR176982 Sequence
19	10.4	74.3	24	6 AR197992	AR197992 Sequence
20	10.4	74.3	24	6 AX190945	AX190945 Sequence
21	10.4	74.3	25	6 AX029401	AX029401 Sequence
22	10.4	74.3	25	6 AX029413	AX029413 Sequence
23	10.4	74.3	31	6 AR024414	AR024414 Sequence
24	10.4	74.3	31	6 AR091787	AR091787 Sequence
25	10.4	74.3	31	6 AX248592	AX248592 Sequence
26	10.4	74.3	31	6 I71206	I71206 Sequence
27	10.4	74.3	31	6 I83765	I83765 Sequence
28	10.4	74.3	32	6 A57190	A57190 Sequence
29	10.4	74.3	45	6 AR083218	AR083218 Sequence
30	10.4	74.3	45	6 AR083219	AR083219 Sequence
31	10.4	74.3	45	6 AR198841	AR198841 Sequence
32	10.4	74.3	47	6 AX194743	AX194743 Sequence
33	10	71.4	20	6 AX329418	AX329418 Sequence
34	10	71.4	20	6 AX443214	AX443214 Sequence
35	10	71.4	20	6 AX452324	AX452324 Sequence
36	10	71.4	21	6 AR210393	AR210393 Sequence
37	10	71.4	23	6 A30274	A30274 Nisin 2'-PCR
38	10	71.4	23	6 I33945	I33945 Sequence
39	10	71.4	24	6 AR090423	AR090423 Sequence
40	10	71.4	24	6 AR197458	AR197458 Sequence
41	10	71.4	24	6 AX447309	AX447309 Sequence
42	10	71.4	25	6 AX042600	AX042600 Sequence
43	10	71.4	25	6 AX201537	AX201537 Sequence
44	10	71.4	26	6 AX037879	AX037879 Sequence
45	10	71.4	26	6 AX110848	AX110848 Sequence

#### ALIGNMENTS

RESULT 1

AX190063

LOCUS

Sequence 242 from Patent WO0147942.

AX190063

AX190063.1 GI:15143435

DEFINITION

AX190063

ACCESSION

AX190063

VERSION

AX190063.1 GI:15143435

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 50)

REFERENCE

Shinkets,R.A. and Leach,M.

TITLE

Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

JOURNAL Patent: WO 0147942-A 242 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
Source 1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/note="2 of 2 allelic variants (241 is other entry)"  
misc\_feature 25..26  
Accession number cg43982025"  
BASE COUNT 9 a 13 c 21 g 7 t  
ORIGIN

Query Match 81.4%; Score 11.4; DB 6; Length 50;  
Best Local Similarity 85.7%; Pred. No. 6.6e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCCA 14  
||||| 1111  
19 CCAGGTGCAGGCCA 32

Db

RESULT 2  
AX190065 50 bp DNA linear PAT 08-AUG-2001  
LOCUS  
DEFINITION Sequence 244 from Patent WO0147942.  
ACCESSION AX190065  
VERSION AX190065.1 GI:15143437  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Shinkets, R.A. and Leach, M.  
TITLE Nucleic acids containing single nucleotide polymorphisms and  
methods of use thereof  
JOURNAL Patent: WO 0147942-A 244 05-JUL-2001;  
Curagen Corporation (US)  
FEATURES Location/Qualifiers  
Source 1..50  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/note="2 of 2 allelic variants (243 is other entry)"  
misc\_feature 25..26  
Accession number cg43982025"  
BASE COUNT 9 a 13 c 21 g 7 t  
ORIGIN

Query Match 81.4%; Score 11.4; DB 6; Length 50;  
Best Local Similarity 85.7%; Pred. No. 6.6e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCCA 14  
||||| 1111  
18 CCAGGTGCAGGCCA 31

Db

RESULT 3  
AR179980/c 15 bp DNA linear PAT 20-APR-2002  
LOCUS  
DEFINITION Sequence 48 from patent US 6333152.  
ACCESSION AR179980  
VERSION AR179980.1 GI:20222013  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W.  
TITLE Gene expression profiles in normal and cancer cells  
JOURNAL Patent: US 6333152-A 48 25-DEC-2001;

FEATURES Location/Qualifiers  
Source 1..15  
/organism="unknown"  
BASE COUNT 3 a 5 c 3 g 4 t  
ORIGIN

Query Match 78.6%; Score 11; DB 6; Length 15;  
Best Local Similarity 91.7%; Pred. No. 1.3e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGGTGTAGNCCA 14  
||||| 1111  
14 AGGTGTAGGCCA 3

Db

RESULT 4  
AX249591/c 31 bp DNA linear PAT 28-SEP-2001  
LOCUS  
DEFINITION Sequence 1670 from Patent WO0166800.  
ACCESSION AX249591  
VERSION AX249591.1 GI:15864214  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.  
TITLE Human single nucleotide polymorphisms  
JOURNAL Patent: WO 0166800-A 1670 13-SEP-2001;  
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)  
FEATURES Location/Qualifiers  
Source 1..31  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 7 a 8 c 9 g 6 t 1 others  
ORIGIN

Query Match 78.6%; Score 11; DB 6; Length 31;  
Best Local Similarity 91.7%; Pred. No. 1.2e+05;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGGTGTAGNCC 13  
||||| 1111  
14 CAGGTGTAGGCC 3

Db

RESULT 5  
AR132395/c 15 bp DNA linear PAT 16-MAY-2001  
LOCUS  
DEFINITION Sequence 820 from patent US 6194150.  
ACCESSION AR132395  
VERSION AR132395.1 GI:14121300  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb, D.T., Jarvis, T. and McSwiggen, J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 820 27-FEB-2001;  
FEATURES Location/Qualifiers  
Source 1..15  
/organism="unknown"

BASE COUNT 3 a 4 c 5 g 3 t  
ORIGIN

Query Match 74.3%; Score 10.4; DB 6; Length 15;  
Best Local Similarity 84.6%; Pred. No. 2.9e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13  
||||| 1111

Db 15 CCAGGTGAGTCC 3

RESULT 6  
LOCUS ARI32396/c 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 821 from patent US 6194150.  
ACCESSION ARI32396  
VERSION ARI32396.1 GI:14121301  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 821 27-FEB-2001;  
FEATURES  
source 1.15  
/organism="unknown"  
BASE COUNT 3 a 4 c 5 g 3 t  
ORIGIN

Query Match 74.3%; Score 10.4; DB 6; Length 15;  
Best Local Similarity 84.6%; Pred. No. 2.9e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13  
14 CCAGGTGAGTCC 2

Db 14 CCAGGTGAGTCC 2

RESULT 7  
LOCUS AB067924/c 18 bp DNA linear SYN 08-AUG-2001  
DEFINITION Synthetic construct DNA, forward primer for human STS-sts627405 at 1p36.  
ACCESSION AB067924  
VERSION AB067924.1 GI:15128728  
KEYWORDS  
SOURCE synthetic construct DNA.  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,  
Matanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,  
Mochizuki,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.  
and Soeda,E.  
TITLE A BAC-based STS-content map spanning a 35-Mb region of human  
JOURNAL Genomics 74 (1), 55-70 (2001)  
MEDLINE 21269192  
REFERENCE 2 (bases 1 to 18)  
AUTHORS Horii,A.  
TITLE Direct Submission  
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of  
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,  
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,  
Tel:81-22-717-8042, Fax:81-22-717-8047)  
FEATURES  
source 1.18  
Location/Qualifiers  
misc\_feature 1.18  
/organism="synthetic construct"  
/db xref="taxon:32630"

BASE COUNT 3 a 5 c 7 g 3 t  
ORIGIN

Query Match 74.3%; Score 10.4; DB 12; Length 18;  
Best Local Similarity 84.6%; Pred. No. 2.9e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13  
14 CCAGGTGAGTCC 2

Db 14 CCAGGTGAGTCC 2

RESULT 8  
LOCUS AX027079/c 19 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 37 from Patent WO0040719.  
ACCESSION AX027079  
VERSION AX027079.1 GI:1018094  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Bonthron,D. and Markham,A.F.  
TITLE Wound healing and orofacial clefting  
JOURNAL Patent: WO 0040719-A 37 13-JUL-2000;  
BONTHRON DAVID (GB) ; UNIV LEEDS (GB) ; MARKHAM ALEXANDER FRED (GB)  
FEATURES  
source 1.19  
Location/Qualifiers  
misc\_feature 1.19  
/organism="Homo sapiens"  
/db xref="taxon:9606"  
/note="Oligonucleotide primer"

BASE COUNT 4 a 7 c 5 g 3 t  
ORIGIN

Query Match 74.3%; Score 10.4; DB 6; Length 19;  
Best Local Similarity 84.6%; Pred. No. 2.8e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13  
13 CCAGGTGAGTCC 1

Db 13 CCAGGTGAGTCC 1

RESULT 9  
LOCUS BOVDIK06 20 bp DNA linear MM 09-FEB-1999  
DEFINITION Bovine DNA, microsatellite DIK015 PCR antisense primer.  
ACCESSION D44507  
VERSION D44507.1 GI:624797  
KEYWORDS microsatellite.  
SOURCE Bos taurus DNA.  
ORGANISM Bos taurus  
REFERENCE 1 (sites)  
AUTHORS Hirano,T., Nakane,S., Watanabe,T., Takeda,H.,  
Yamakuchi,H., Morita,M., Barendse,W. and Sugimoto,Y.  
TITLE Five bovine polymorphic dinucleotide microsatellite loci (DIK008,  
DIK010, DIK015, DIK016 and DIK020)  
JOURNAL Anim. Genet. 26 (6), 447-448 (1995)  
MEDLINE 96151440  
REFERENCE 2 (sites)  
AUTHORS Hirano,T., Nakane,S., Mizoshita,K., Yamakuchi,H.,  
Inoue-Murayama,M., Watanabe,T., Barendse,W. and Sugimoto,Y.  
TITLE Characterization of 42 highly polymorphic bovine microsatellite  
markers  
JOURNAL Anim. Genet. 27 (5), 365-368 (1996)  
MEDLINE 97083737  
REFERENCE 3 (bases 1 to 20)  
AUTHORS Inoue,M., Watanabe,T., Hirano,T., Yamakuchi,H.,  
Watanabe,E., Morita,M. and Sugimoto,Y.  
TITLE Isolation of microsatellites from Japanese black cattle (Wagyu) and  
their application to individual identification and paternity  
exclusion  
JOURNAL Unpublished  
REFERENCE 4 (bases 1 to 20)

AUTHORS	Sugimoto, Y.
TITLE	Direct Submission
JOURNAL	Submitted (21-DEC-1994)
	Yoshikazu Sugimoto, Japan Live Stock

Submitted (21-DEC-1994) Yoshihazu Sugimoto, Japan Liv  
Technology Association, Shiraoka Institute of Animal  
Nishigo Odakura, Nishishirakawa, Fukushima 961, Japan  
(E-mail: LDIO3222@niftyserve.or.jp, Tel: 0248-25-5641,  
Fax: 0248-25-5725)

FEATURES	Location/qualifiers
source	1. . 20

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/organism="Bos taurus"
/db_xref="taxon:9913"
<1. .20
misc_feature

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BASE COUNT      7 a      4 c      6 g      3 t
ORIGIN
/note="microsatellite D1K015 PCR antisense primer"

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Query Match	74.3%	Score 10.4;	DB 4;	Length 20;
Best Local Similarity	84.6%	Pred. No. 2.8e+05;		
Matches : 11; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY	2	CAGGTGTAGNCCA	14
Db	7	CAGGTGTGCTCCA	19

RESULT	10
AR099541	
LOCUS	AR099541
DEFINITION	Sequence 68 from patent US 6077833.
ACCESSION	AR099541
VERSION	AR099541.1
GI:	GI:12809307
PAT	PAT 14-FEB-2001
linear	

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
Unknown.	Unknown.	Unclassified.	1 (bases 1 to 20)	Bennett,C.Frank. and Vickers,T.A.	oligonucleotide	compositions and methods for the modulation of the expression of B7 protein
				Patent: US 6077833-A	68	20-JUN-2000; Location/Qualifiers

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source      1. 20
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BASE COUNT  4 a      7 c      5 g
ORIGIN

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Query Match	74.38;	Score 10.4;	DB 6;	Length 20;
Best Local Similarity	84.68;	Pred. No. 2.8e+05;		
Matches 11; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY	1	CCAGGTGTAGNCC	13
Db	2	CCAGGTGAAGTCC	14

RESULT	11
ARI16442	
LOCUS	ARI16442
DEFINITION	Sequence 61 from patent US 6218510.
ACCESSION	ARI16442
VERSION	ARI16442.1 GI:15109631
DNA	linear
PAT	08-AUG-2001

SOURCE ORGANISM

REFERENCE 1 (bases 1 to 20)  
AUTHORS Sharpe, A.H., Borriello, F., Freeman, G.J. and Nadler, L.M.  
TITLE B7-1 and B7-2 polypeptides  
JOURNAL Patent: US 6218510-A 61 17-APR-2001;

## FEATURES

### source

BASE COUNT	5 a	6 c	5 g	4 t
	/organism="unknown"			

## ORIGIN

Query Match	74.3%	Score 10.4;	DB 6;	Length 20;
Best Local Similarity	84.6%	Pred. No. 2.8e+05;		
Matches 11; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	CCAGGTGTAGNCC	13
Db	1	CCAGGTGAAGTCC	13

RESULT	12
LOCUS	ARI78822
DEFINITION	ARI78822 20 bp -DNA- linear PAT 20-APR-2002
Sequence	68 from patent US 6319906.
Accession	AF010003

VERSION	AR178822.1	GI:20219960
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unknown.	

REFERENCE	1 (bases 1 to 20)
AUTHORS	Bennett,C.Frank, and Vickers,T.A.
TITLE	Oligonucleotide compositions and methods for the modulation of the expression of B7 protein
JOURNAL	Patent: US 6319906-A 68-20-NOV-2001;
FEATURES	Location/Qualifiers

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BASE COUNT      4 a      7 c      5 g      4 t
ORIGIN          /organism="unknown"
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Query Match	74.3%	Score 10.4;	DB 6;	Length 20;
Best Local Similarity	84.6%;	Pred. No. 2.8e+05;		
Matches	11;	Conservative	0;	Mismatches. 2;
			Indels	0;
			Gaps	0;

QY	1	CCAGGTGTAGNCC	13
.			
Db	2	CCAGGTGAAGTCC	14

RESULT 13			
AX298604			
LOCUS	20 bp	DNA	
AX298604			
DEFINITION	Sequence 238 from Patent WO0183749.	Linear	PAT 26-NOV-2001
DESCRIPTION	AX298604		

KEYWORDS	.
SOURCE	Mus sp.
ORGANISM	Mus sp.

REFERENCE  
1. Eumariota; Metazoa; Chordata; Crinata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS  
Bachmanov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S., Li, X., Ohmen, J.D., Reed, D.R., Ross, D., and Tordoff, M.G.  
TITLE  
Gene and sequence variation associated with sensing carbohydrate compounds and other sweeteners  
JOURNAL  
Patent: WO 0183749-A 238 08-NOV-2001;  
WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center (US)

FEATURES	Location/Qualifiers
source	1. .20

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BASE COUNT      6 a      5 c      6 g      3 t
ORIGIN          /db_xref="taxon:10095"
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Query Match	74.3%	Score 10.4;	DB 6;	Length 20;
Best Local Similarity	84.6%	Pred. No. 2.8e+05;		
Matches 11; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 2 CAGGTGTAGNCCA 14  
||| ||||| |||



Db 4 CAGGTGTAGACCA 16

RESULT 14  
AB068080/c 20 bp DNA linear SYN 06-AUG-2001  
LOCUS Synthetic construct DNA, forward primer for human STS-R272C15F  
DEFINITION at 1p36.  
ACCESSION AB068080  
VERSION AB068080.1 GI:15128884  
KEYWORDS  
SOURCE synthetic construct DNA.  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
1  
Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,  
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,  
Morishashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.  
and Soeda, E.  
A BAC-based STS-content map spanning a 35-Mb region of human  
chromosome 1p35-p36  
Genomics 74 (1), 55-70 (2001)

TITLE  
JOURNAL  
MEDLINE  
REFERENCE  
2 (bases 1 to 20)  
Hori, A.  
TITLE  
JOURNAL  
Direct Submission  
Submitted (04-AUG-2001) Akira Hori, Tohoku University School of  
Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai,  
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,  
Tel:81-22-717-8042, Fax:81-22-717-8047)  
Location/Qualifiers  
1. 20  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

misc-feature  
1. 20  
/note="forward primer for human STS-R272C15F at 1p36  
STS-R272C15F obtained from clones B359F10, B272C15,  
B91D18, Human BAC library RPCI-11"

BASE COUNT 1 4 a 4 c 6 g 6 t  
ORIGIN

Query Match 74.3%; Score 10.4; DB 12; Length 20;  
Best Local Similarity 84.6%; Pred. No. 2.8e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCC 13  
|||||  
Db 14 CCAGGTATAGCCC 2

RESULT 15  
AX180631/c 22 bp DNA linear PAT 06-AUG-2001  
LOCUS AX180631  
DEFINITION Sequence 209 from Patent WO0146391.  
ACCESSION AX180631  
VERSION AX180631.1 GI:15132517  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
artificial sequences.  
1 (bases 1 to 22)  
REFERENCE  
AUTHORS Osbourne, A. E., Haralampidis, K. and Bryan, G. T.  
TITLE Plant gene  
JOURNAL Patent: WO 0146391-A 209 28-JUN-2001;  
Plant Bioscience Limited (GB)  
FEATURES  
Location/Qualifiers  
1. 22  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Primer"

BASE COUNT 1 5 a 6 c 4 g 7 t  
ORIGIN

Query Match 74.3%; Score 10.4; DB 6; Length 22;  
Best Local Similarity 84.6%; Pred. No. 2.8e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CAGGTGTAGNCCA 14  
|||||  
Db 18 CAGGTGTAGACCA 6

Search completed: June 21, 2003, 22:14:39  
Job time : 285.094 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:51; Search time 76.7812 Seconds

(Without alignments)  
410.621 Million cell updates/sec

Title: US-09-964-666-13

Perfect score: 14

Sequence: 1 CCAGCTGTAGNCCA 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT: \*  
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22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT: \*  
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT: \*  
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11.4	81.4	50	22	AAH90362 Human clone cg4398
2	11.4	81.4	50	22	AAH90364 Human clone cg4398
3	11.4	78.6	15	20	AAAX0994 Tag sequence of a
4	11.4	78.6	15	24	ABK31947 Human colon cancer
5	11.4	78.6	31	22	AAI31182 Human single nucle
6	10.4	74.3	15	17	AAK65326 Mouse B7-1 hammet
7	10.4	74.3	15	17	AAK65327 Mouse B7-1 hammet
8	10.4	74.3	15	24	ABLS2004 Human SLC18A2 alle
9	10.4	74.3	18	20	AAK84480 PCR primer for Hum

Result ID	Score	Query Match	Length	DB ID	Description
10	10.4	74.3	18	21	AAK52824 Human CD44 antisen
11	10.4	74.3	18	24	ABLA3601 Human chromosome 1
12	10.4	74.3	19	21	AAK58857 Oligonucleotide us
13	10.4	74.3	20	16	AAAT01071 Mouse B7-1 (alt)en
14	10.4	74.3	20	19	AAV48029 Murine B7-1 target
15	10.4	74.3	20	21	AAAG1878 Antisense primer t
16	10.4	74.3	20	22	AAK3148 Oligonucleotide fo
17	10.4	74.3	20	22	AAK32871 Murine B7-1 mRNA a
18	10.4	74.3	20	24	AAK34980 Human MTHFR gene c
19	10.4	74.3	20	24	AAK56640 Telomerase reverse
20	10.4	74.3	20	24	AAK59628 Murine SAC1 gene-s
21	10.4	74.3	20	24	ABLA4107 Human chromosome 1
22	10.4	74.3	20	24	ABLA5384 Human chromosome 2
23	10.4	74.3	21	17	AAK11230 Internal control p
24	10.4	74.3	21	19	AAK21625 Human patched (ptc
25	10.4	74.3	21	21	AAK59964 PCR primer for thr
26	10.4	74.3	22	22	AAK59815 Oat Beta-amylin sy
27	10.4	74.3	24	17	AAK34014 Mycobacteria 16S-2
28	10.4	74.3	24	24	ABK66989 Human gene specif
29	10.4	74.3	25	20	AAK34310 Human oestrogen re
30	10.4	74.3	27	18	AAK55516 Oligonucleotide 35
31	10.4	74.3	27	18	AAK62986 c-mp1 receptor/ago
32	10.4	74.3	27	19	AAK55428 Primer 35-5' for c
33	10.4	74.3	29	24	ABK87566 Matrix metalloprot
34	10.4	74.3	30	18	AAK97150 Primer S1 for ob p
35	10.4	74.3	31	22	AAI30183 Human single nucle
36	10.4	74.3	32	17	AAK33447 MAB chm1n5 light
37	10.4	74.3	33	24	AAK171477 Human pax protein
38	10.4	74.3	37	20	AAK89404 Downstream PCR pri
39	10.4	74.3	39	19	AAV17107 CLK serine/threoni
40	10.4	74.3	45	16	AAK94195 Transmembrane olig
41	10.4	74.3	45	16	AAK94195 Transmembrane olig
42	10.4	74.3	45	20	AAK88230 Nucleotide sequenc
43	10.4	74.3	45	21	AAK53225 Human G-protein co
44	10.4	74.3	47	20	AAK15861 PCR primer used to
45	10.4	74.3	47	20	AAK15863 PCR primer used to

# ALIGNMENTS

RESULT 1  
AAH90362  
ID AAH90362 standard; CDNA: 50 BP.  
AC AAH90362;  
DT 08-OCT-2001 (first entry)  
XX  
DE Human clone cg43982025 SNP site, SEQ ID NO:242.  
XX  
KW Human: single nucleotide polymorphism; SNP; chromosome 19;  
KW detection; identification; gene therapy; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
FH key Location/Qualifiers  
FT Variation replace(25..26,GCC)  
FT /\*tag=a  
FT /standard\_name="single nucleotide polymorphism"  
XX  
PN WO200147942-A2.  
XX  
PD 05-JUL-2001.  
XX  
PF 27-DEC-2000; 2000WO-US53387.  
XX  
PR 27-DEC-1999; 99US-0472865.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shimkels RA, Leach M;  
XX

DR WPI; 2001-425617/45.  
 XX  
 PT New polynucleotides containing single nucleotide polymorphisms, for  
 PT detecting the presence of polymorphism, detecting a polymorphic site,  
 PT and treating a patient suffering from a pathology ascribed to the  
 PT polymorphism

Claim 1; Page 87; 295pp; English.

XX  
 PS Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which  
 CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to  
 CC 568 (AAH90121-AAH90688) are consecutive pairs of nucleotides which  
 CC contain silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are  
 CC consecutive pairs of nucleotides containing SNPs which result in changes  
 CC in the corresponding amino acid sequences (AAG64751-AAG64762). The SNPs  
 CC in sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino  
 CC acid changes, while those in sequences 575 to 578 (AAH90695-AAH90698)  
 CC result in non-conservative changes. The SNP in sequences 579 and 580  
 CC (AAH90699-AAH90700) generates a frameshift mutation. The invention also  
 CC relates to a method of detecting a polymorphic site in a nucleic acid and  
 CC a method of determining the relatedness of two nucleic acids. It also  
 CC encompasses peptides containing polymorphic sites, antibodies raised  
 CC against such peptides, and a method of detecting polymorphic proteins/  
 CC peptides using the antibodies. The nucleic acids are useful for gene  
 CC therapy of an individual having, suspected of having, or at risk of  
 CC developing a pathological condition due to the presence of a sequence  
 CC polymorphism. Such treatment would comprise administration of the  
 CC wild-type nucleic acid sequence. Antibodies raised against polymorphic  
 CC peptides can also be used in the treatment of such individuals.

XX SO Sequence 50 BP; 9 A; 13 C; 21 G; 7 T; 0 other:

Query Match 81.4%; Score 11.4; DB 22; Length 50;  
 Best Local Similarity 85.7%; Pred. No. 3.6e+03;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCCA 14  
 ||||||| 11111  
 Db 19 CCAGGTGCAGGCCA 32

#### RESULT 2

AAH90364  
 ID AAH90364 standard; cDNA; 50 BP.

XX AAH90364;

DT 08-OCT-2001 (first entry)

DE Human clone c943982025 SNP site, SEQ ID NO:244.

XX Human; single nucleotide polymorphism; SNP; chromosome 19;  
 KW detection; identification; gene therapy; genetic disorder; ss.

XX Homo sapiens.

OS  
 XX Key Location/Qualifiers  
 FH replace(25..26,CCA)  
 FT /\*tag-a  
 FT /standard\_name="single nucleotide polymorphism"

XX WO200147942-A2.

XX 05-JUL-2001.

XX 27-DEC-2000; 2000MO-US5387.

XX 27-DEC-1999; 99US-0472865.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

DR WPI; 2001-425617/45.  
 XX  
 PT New polynucleotides containing single nucleotide polymorphisms, for  
 PT detecting the presence of polymorphism, detecting a polymorphic site,  
 PT and treating a patient suffering from a pathology ascribed to the  
 PT polymorphism

Claim 1; Page 87; 295pp; English.

XX  
 PS Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which  
 CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to  
 CC 568 (AAH90121-AAH90688) are consecutive pairs of nucleotides which  
 CC contain silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are  
 CC consecutive pairs of nucleotides containing SNPs which result in changes  
 CC in the corresponding amino acid sequences (AAG64751-AAG64762). The SNPs  
 CC in sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino  
 CC acid changes, while those in sequences 575 to 578 (AAH90695-AAH90698)  
 CC result in non-conservative changes. The SNP in sequences 579 and 580  
 CC (AAH90699-AAH90700) generates a frameshift mutation. The invention also  
 CC relates to a method of detecting a polymorphic site in a nucleic acid and  
 CC a method of determining the relatedness of two nucleic acids. It also  
 CC encompasses peptides containing polymorphic sites, antibodies raised  
 CC against such peptides, and a method of detecting polymorphic proteins/  
 CC peptides using the antibodies. The nucleic acids are useful for gene  
 CC therapy of an individual having, suspected of having, or at risk of  
 CC developing a pathological condition due to the presence of a sequence  
 CC polymorphism. Such treatment would comprise administration of the  
 CC wild-type nucleic acid sequence. Antibodies raised against polymorphic  
 CC peptides can also be used in the treatment of such individuals.

XX SO Sequence 50 BP; 9 A; 13 C; 21 G; 7 T; 0 other:

Query Match 81.4%; Score 11.4; DB 22; Length 50;  
 Best Local Similarity 85.7%; Pred. No. 3.6e+03;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCCA 14  
 ||||||| 11111  
 Db 18 CCAGGTGCAGGCCA 31

#### RESULT 3

AAH30994/c  
 ID AAH30994 standard; DNA; 15 BP.

XX AAH30994;

DT 21-MAY-1999 (first entry)

DE Tag sequence of a transcript increased in colorectal cancer.

XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;  
 KW diagnosis; prognosis; treatment; ss.

XX Homo sapiens.

XX WO9853319-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98MO-US10277.

XX 21-MAY-1997; 97US-0047352.

XX (UYJO ) UNIV JOHNS HOPKINS.

XX Kinzler KW, Vogelstein B;

XX WPI; 1999-070161/06.

XX Use of isolated gene transcripts - useful for developing products  
 PT for the diagnosis, prognosis and treatment of cancers, particularly  
 PT colon and pancreatic cancer

XX Claim 2; Page 24; 120pp; English.  
PS  
XX AAX30947-31815 represent tag sequences of transcripts that are  
CC differentially expressed in colorectal cancer, in pancreatic  
CC cancer, or in both. The tag sequences can be used to identify  
CC genes by matching the tag to a gen data base member, or by using  
CC the tag sequences as probes to isolate unidentified genes from  
CC cDNA libraries. The tag sequences can also be used in a method  
CC for diagnosing colon or pancreatic cancer in a sample suspected  
CC of being neoplastic. The method comprises comparing the level of  
CC at least one transcript in a first sample of a tissue to a second  
CC sample, where the first sample is a colonic tissue suspected of  
CC being neoplastic and the second sample is a normal human colonic  
CC tissue. The transcript is identified by a tag selected from  
CC AAX30947-31815. The methods of the invention can be used in the  
CC diagnosis, prognosis and treatment of cancer.  
XX  
SQ Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 other;  
Query Match 78.6%; Score 11; DB 20; Length 15;  
Best Local Similarity, 91.7%; Pred. No. 5.8e+03;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 AGGTGTAGNCCA 14  
Db 14 AGGTGTAGCCCA 3  
RESULT 4  
ABK31947/c  
ID ABK31947 standard; DNA: 15 BP.  
AC ABK31947;  
XX 23-APR-2002 (first entry)  
DT  
XX Human colon cancer SAGE tag #48.  
DE  
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;  
KM serial analysis of gene expression; diagnostic; prognostic; probe;  
KW cancer marker; ss.  
XX  
XX Homo sapiens.  
OS  
XX US6333152-B1.  
PN  
XX 25-DEC-2001.  
PD  
XX 20-MAY-1998; 98US-0081646.  
PF  
XX 20-MAY-1998; 98US-0081646.  
PR  
XX 20-MAY-1998; 98US-0081646.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;  
DR WPI; 2002-153821/20.  
XX  
XX New human nucleic acid containing specific SAGE tags, useful as  
PT diagnostic markers for cancer, also derived probes  
PS  
XX Disclosure; Column 15; 161pp; English.  
XX The invention relates to an isolated, purified human nucleic acid (1)  
CC that has the same sequence as a mRNA found in humans and is a SAGE  
CC (serial analysis of gene expression) tag comprising a single stranded  
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are  
CC diagnostic and prognostic markers of cancer, especially of the colon and  
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer  
CC SAGE tags of the invention.  
XX  
SQ Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 other;

Query Match 78.6%; Score 11; DB 24; Length 15;  
Best Local Similarity 91.7%; Pred. No. 5.8e+03;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 AGGTGTAGNCCA 14  
Db 14 AGGTGTAGCCCA 3  
RESULT 5  
AA131182/c  
ID AA131182 standard; DNA: 31 BP.  
XX  
AC AA131182;  
DT  
XX 18-OCT-2001 (first entry)  
DE  
XX Human single nucleotide polymorphism (SNP) 255.  
DE  
XX  
KM Human; resequence; genotype; disease; forensic; paternity testing;  
KM single nucleotide polymorphism; SNP; ss.  
XX  
OS Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FH replace(16,T)  
FT Variation /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism"  
WO200166800-A2.  
PD 13-SEP-2001.  
XX  
XX 07-MAR-2001; 2001WO-US07268.  
PF  
XX 07-MAR-2000; 2000US-0187510.  
PR 22-MAY-2000; 2000US-0206129.  
XX  
PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
XX  
XX Cargill M, Ireland JS, Lander ES;  
PI  
XX WPI; 2001-522952/57.  
DR  
XX  
XX Nucleic acid molecules from the human genome which include polymorphic  
PT sites, useful in methods for predicting the presence, absence or  
PT severity of a particular phenotype or disorder (e.g. diabetes)  
PT associated with a particular genotype  
XX  
PS Claim 1; Page 132; 145pp; English.  
XX  
XX The invention relates to the identification of nucleic acid molecules  
CC (AA129513-AA13114) from the human genome which include polymorphic sites  
CC which can predispose individuals to disease. Various genes from a number  
CC of individuals were resequenced and single nucleotide polymorphisms  
CC (SNPs) in these genes discovered. The method is useful for predicting the  
CC presence, absence or severity of a particular phenotype or disorder (e.g.  
CC diabetes) associated with a particular genotype. The nucleic acids  
CC containing the polymorphic sites may be useful in forensics and paternity  
CC testing.  
XX  
SQ Sequence 31 BP; 8 A; 8 C; 9 G; 6 T; 0 other;  
Query Match 78.6%; Score 11; DB 22; Length 31;  
Best Local Similarity 91.7%; Pred. No. 6e+03;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 CAGGTGTAGNCC 13  
Db 14 CAGGTGTAGACC 3

RESULT 6  
AA65326/c  
ID AAX65326 standard; RNA; 15 BP.  
XX  
XX AAX65326;  
XX  
XX 20-JUL-1999 (first entry)  
XX  
XX Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1958.  
XX  
XX Arthritic condition; graft tolerance; immune response; target; cleavage;  
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
XX stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
XX diagnosis; ss.  
XX  
XX Mus sp.  
XX  
XX WO9618736-A2.  
XX  
XX 20-JUN-1996.  
XX  
XX 22-NOV-1995; 95WO-US15516.  
XX  
XX 05-OCT-1995; 95US-0541365.  
XX 13-DEC-1994; 94US-0354920.  
XX 23-DEC-1994; 94US-0363253.  
XX 23-DEC-1994; 94US-0363254.  
XX 17-FEB-1995; 95US-0390850.  
XX 20-APR-1995; 95US-0426124.  
XX 02-MAY-1995; 95US-0432874.  
XX 04-MAY-1995; 95US-0434509.  
XX 07-JUL-1995; 95US-0000951.  
XX 07-JUL-1995; 95US-0000974.  
XX 07-AUG-1995; 95US-0512861.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;  
XX Belgelman L, Karpelsky A, Modak A, Usman N, Burgin A;  
XX Metulic-Adamic J, Jarvis T, Thompson JD, Wincott F;  
XX WPI: 1996-300653/30.  
XX  
XX Enzymatic nucleic acid molecules having a hammer-head motif - used  
XX for the treatment of arthritis, induction of graft tolerance or  
XX treatment of auto-immune diseases  
XX  
XX Claim 10; Page 179; 307pp; English.  
XX  
XX The present invention describes a novel enzymatic nucleic acid (ENA)  
XX having a hammerhead motif (HM) comprising: (i) at least 5 ribose  
XX residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)  
XX at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.  
XX The ENA's can inhibit collagenase and stromelysin production in the  
XX synovial membrane of joints for the treatment or prevention of arthritis,  
XX particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
XX be used to treat antigen presenting cells of a donor to induce tolerance  
XX in a recipient to an allantigen of a donor. They can also be used for  
XX enhancing graft tolerance or for treating autoimmune disease, and for  
XX treating allergies and other inflammatory conditions. The ENA's can also  
XX be used in diagnosis. Ribozyme therapy impacts on the expression of  
XX stromelysin without introducing the non-specific effects upon gene  
XX expression which accompany treatment with retinoids and dexamethasone.  
XX The concentration of ribozyme required to affect a therapeutic treatment  
XX is lower than that required of antisense molecules, and is highly  
XX specific. The present sequence is used in the exemplification of the  
XX present invention.  
XX  
XX Sequence 15 BP; 3 A; 4 C; 5 G; 3 U; 0 other;  
XX  
XX Query\_Match 74.3%; Score 10.4; DB 17; Length 15;  
XX Best\_Local\_Similarity 84.6%; Pred. No. 1.3e+04;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCAGGTGAGGCC 13  
|||||11111111  
Db 15 CCAGGTGAGTCC 3  
RESULT 7  
AA65327/c  
ID AAX65327 standard; RNA; 15 BP.  
XX  
XX AAX65327;  
XX  
XX 20-JUL-1999 (first entry)  
XX  
XX Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1959.  
XX  
XX Arthritic condition; graft tolerance; immune response; target; cleavage;  
XX hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
XX stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
XX rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
XX diagnosis; ss.  
XX  
XX Mus sp.  
XX  
XX WO9618736-A2.  
XX  
XX 20-JUN-1996.  
XX  
XX 22-NOV-1995; 95WO-US15516.  
XX  
XX 05-OCT-1995; 95US-0541365.  
XX 13-DEC-1994; 94US-0354920.  
XX 23-DEC-1994; 94US-0363253.  
XX 23-DEC-1994; 94US-0363254.  
XX 17-FEB-1995; 95US-0390850.  
XX 20-APR-1995; 95US-0426124.  
XX 02-MAY-1995; 95US-0432874.  
XX 04-MAY-1995; 95US-0434509.  
XX 07-JUL-1995; 95US-0000951.  
XX 07-JUL-1995; 95US-0000974.  
XX 07-AUG-1995; 95US-0512861.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;  
XX Belgelman L, Karpelsky A, Modak A, Usman N, Burgin A;  
XX Metulic-Adamic J, Jarvis T, Thompson JD, Wincott F;  
XX WPI: 1996-300653/30.  
XX  
XX Enzymatic nucleic acid molecules having a hammer-head motif - used  
XX for the treatment of arthritis, induction of graft tolerance or  
XX treatment of auto-immune diseases  
XX  
XX Claim 10; Page 179; 307pp; English.  
XX  
XX The present invention describes a novel enzymatic nucleic acid (ENA)  
XX having a hammerhead motif (HM) comprising: (i) at least 5 ribose  
XX residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)  
XX at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.  
XX The ENA's can inhibit collagenase and stromelysin production in the  
XX synovial membrane of joints for the treatment or prevention of arthritis,  
XX particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
XX be used to treat antigen presenting cells of a donor to induce tolerance  
XX in a recipient to an allantigen of a donor. They can also be used for  
XX enhancing graft tolerance or for treating autoimmune disease, and for  
XX treating allergies and other inflammatory conditions. The ENA's can also  
XX be used in diagnosis. Ribozyme therapy impacts on the expression of  
XX stromelysin without introducing the non-specific effects upon gene  
XX expression which accompany treatment with retinoids and dexamethasone.  
XX The concentration of ribozyme required to affect a therapeutic treatment  
XX is lower than that required of antisense molecules, and is highly

CC specific. The present sequence is used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 15 BP; 3 A; 4 C; 5 G; 3 U; 0 other;  
XX  
Query Match 74.3%; Score 10.4; DB 17; Length 15;  
Best Local Similarity 84.6%; Pred. No. 1.3e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCAGGTGTAGNCC 13  
Db 14 CCAGGTGAGTCC 2  
XX  
RESULT 8  
ABLS2004/C  
ID ABL52004 standard; DNA; 15 BP.  
XX  
AC ABL52004;  
XX  
DT 11-JUL-2002 (first entry)  
XX  
DE Human SLC18A2 allele specific oligonucleotide primer SEQ ID NO:52.  
XX  
XX Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;  
KW vesicular monoamine transporter; VMAT2; polymorphic site; SNP;  
KW single nucleotide polymorphism; antiinflammatory; neuroleptic;  
KW haplotyping; genotyping; respiratory inflammatory disease;  
KW neuropsychiatric disorder; monoaminergic brain system; primer; ss.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 14  
FT /tag= a  
FT /note= "polymorphic site indicated by an ambiguity base"  
XX  
XX WO200222652-A2.  
XX  
XX 21-MAR-2002.  
XX  
XX 17-SEP-2001; 2001WO-US42217.  
XX  
XX 15-SEP-2000; 2000US-232895P.  
XX  
XX (GENA-) GENA/ISSANCE PHARM INC.  
XX  
XX Anastasio AE, Han J, Klem SE, Sausker EA;  
PI  
XX  
XX WPI; 2002-393942/42.  
XX  
XX  
XX Novel genetic variants of soluble carrier family 18 (vesicular  
PT monamine), member 2 gene useful for screening drugs to treat diseases  
PT e.g. neuropsychiatric disorders involving monoaminergic brain systems  
XX  
XX  
XX Claim 17; Page 15; 183pp; English.  
XX  
XX The present invention describes an isolated polynucleotide (I) having a  
CC sequence (S1) comprising soluble carrier family 18 (vesicular monoamine),  
CC member 2 (SLC18A2) isogene selected from 49 isogenes with regions of a  
CC sequence (S2) of 40023 bp (see ABL51954), and defined by a corresponding  
CC set of polymorphisms whose locations and identities are given in the  
CC specification, or a sequence (S2) complementary to (S1). (I) has  
CC antiinflammatory and neuroleptic activities, and can be used in gene  
CC therapy. Methods from the present invention can be used for haplotyping  
CC and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known  
CC as the vesicular monoamine transporter (VMAT2). (I) is useful in studying  
CC the expression and function of SLC18A2, and in expressing the SLC18A2  
CC protein for use in screening for candidate drugs to treat diseases  
CC related to SLC18A2 activity and in studying the effect of the variation  
CC on the biological activity of SLC18A2 as well as on the binding affinity  
CC of candidate drugs targeting SLC18A2 for the treatment of respiratory

CC inflammatory diseases such as neuropsychiatric disorders involving  
CC monoaminergic brain systems. The present sequence represents an allele  
CC specific oligonucleotide (ASO) primer for human SLC18A2, which is given  
CC in the present invention.  
XX  
SQ Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 1 other;  
XX  
Query Match 74.3%; Score 10.4; DB 24; Length 15;  
Best Local Similarity 84.6%; Pred. No. 1.3e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 CAGGTGTAGNCCA 14  
Db 13 CAGGTGTGGCCCA 1  
XX  
RESULT 9  
AAx84480  
ID AAX84480 standard; DNA; 18 BP.  
XX  
AC AAX84480;  
XX  
DT 10-SEP-1999 (first entry)  
XX  
DE PCR primer for Human EDIRF II coding sequence.  
XX  
XX Embryo derived interleukin related factor; diagnosis; detection; therapy;  
KW EDIRF-related disease; immune disorder; haematopoietic disorder;  
KW developmental disorder; inflammatory disease; arthritis; psoriasis;  
KW EDIRF II; PCR primer; ss.  
XX  
XX Synthetic.  
XX  
XX Homo sapiens.  
XX  
XX WO932632-A1.  
XX  
XX 01-JUL-1999.  
XX  
XX 18-DEC-1998; 98WO-US27068.  
XX  
XX 19-DEC-1997; 97US-0994890.  
XX  
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
XX  
XX Holtzman DA;  
PI  
XX  
XX WPI; 1999-418929/35.  
XX  
XX Nucleic acid encoding embryo-derived interleukin-related factors  
XX  
XX Example 2; Page 75; 116pp; English.  
XX  
XX This sequence is a PCR primer for DNA encoding the embryo-derived  
CC interleukin-related factor (EDIRF) of the invention, designated human  
CC EDIRF II. The EDIRF DNA and protein sequences (and their homologues),  
CC antibodies (Ab) specific for EDIRF, and other modulators are used:  
CC (i) in screening and detection assays, e.g. for chromosome mapping,  
CC tissue typing or forensic studies; (ii) in diagnosis, prognosis or  
CC monitoring clinical trials; and (iii) for treating or preventing  
CC EDIRF-related diseases (especially immune, haematopoietic,  
CC differentiative, developmental or inflammatory disease, including  
CC arthritis and psoriasis. The EDIRF coding sequence, or its fragments, are  
CC also useful as probes and primers (for detecting related sequences and  
CC disease-associated mutations, also for mutagenesis), for expressing  
CC recombinant EDIRF and as source of antisense, ribozyme and peptide  
CC nucleic acids (for inhibiting translation of EDIRF-derived mRNA. EDIRF is  
CC used to raise Ab (useful for detecting EDIRF, including forms with  
CC aberrant post-translational modification, for affinity purification and  
CC therapeutically) and to screen for specific modulators (e.g. peptides or  
CC peptidomimetics).  
XX  
XX  
XX Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 other;  
XX  
XX

Query Match 74.3%; Score 10.4; DB 20; Length 18;  
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGGTGTAGNCCA 14  
 ||||| ||||  
 Db 3 CAGGTGACAGCCA 15

RESULT 10  
 AAA52824/C  
 ID AAA52824 standard; DNA; 18 BP.

AC AAA52824;

DT 15-SEP-2000 (first entry)

XX Human CD44 antisense oligonucleotide ISIS# 18713.

DE Human: CD44; cell surface adhesion receptor; cytostatic; antirheumatic;

KM antinflammatory; antiarthritic; CD44 antisense inhibition;  
 KM hyperproliferative disorder; cancer; inflammatory disorder;  
 KM rheumatoid arthritis; ss.

OS Homo sapiens.

PN WO200035935-A1.

PD 22-JUN-2000.

PF 14-DEC-1999; 99WO-US29576.

PR 17-DEC-1998; 98US-0213719.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowser LM;

XX WPI: 2000-431564/37.

PT New antisense compound, that inhibits the expression of human cell

PT surface adhesion receptor CD44, for treating hyperproliferative

PT disorders and inflammatory conditions, such as cancer and rheumatoid

PT arthritis -

PS Claim 3; Page 76; 105pp; English.

XX The present sequence is one of a large number of antisense

CC oligonucleotides designed to target different regions of the human CD44

CC mRNA. CD44 is a multifunctional human cell surface adhesion receptor.

CC The oligonucleotides were analysed for effect on CD44 mRNA levels by

CC quantitative real-time PCR analysis. Antisense oligonucleotides that

CC inhibit CD44 expression can be used to treat CD44-associated conditions

CC including hyperproliferative disorders, such as cancer, and inflammatory

CC conditions, such as rheumatoid arthritis. The antisense compounds

CC hybridise to CD44 nucleic acids, thus allowing sandwich and other assays

CC to be easily constructed.

CC Note: The sequence has a phosphorothioate backbone and may be either an

CC oligodeoxynucleotide or a chimeric oligonucleotide containing

CC 2'-methoxyethyl (2'-MOE) wings and a deoxy gap. The ISIS number given

CC above corresponds to the oligodeoxynucleotide sequence.

SO Sequence 18 BP; 6 A; 5 C; 4 G; 3 T; 0 other;

Query Match 74.3%; Score 10.4; DB 21; Length 18;

Best Local Similarity 84.6%; Pred. No. 1.3e+04;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGGTGTAGNCCA 14  
 ||||| ||||  
 Db 16 CAGGTGTATCCA 4

RESULT 11  
 ABL43601/C  
 ID ABL43601 standard; DNA; 18 BP.

AC ABL43601;

DT 11-APR-2002 (first entry)

DE Human chromosome 1p36-35 PCR primer SEQ ID NO:645.

KM Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;

KM genome; PCR primer; ss.

OS Homo sapiens.

PN JP2001321190-A.

PD 20-NOV-2001.

PF 12-MAR-2001; 2001JP-0068285.

PR 10-MAR-2000; 2000JP-0066716.

PA (RIKA) RIKAKAKU KENKYUSHO.

PI (GENO-) GENOTEX YG.

XX WPI: 2002-144136/19.

PT Arraying genome clones -

XX Claim 4; Page 17; 528pp; Japanese.

PS The present invention describes a method of arraying genome clones. The

CC method comprises: (a) clones of the genomic libraries contained in

CC multiwell plates numbered for discrimination are mixed in each of the

CC multiwell plates; (b) a primer designed based on the chromosome marker

CC sequence is added to the mixture to carry out an amplification reaction;

CC (c) a signal corresponding to the marker is detected from the resultant

CC amplified product to specify the discrimination Nos. of the multiwell

CC plates containing the clones having said marker sequence; (d) the order

CC of the markers is changed so that the same discrimination Nos. succeed to

CC the maximum in the specified discrimination Nos. to array the multiwell

CC plates; (e) the clones in the multiwell plates of the specified

CC discrimination Nos. are mixed respectively in each well of longitudinal

CC and lateral directions; (f) the mixed clones are cultured and the

CC resultant cultures are amplified by using the above primer; (g) signals

CC are detected from the amplified products; (h) the clones in the multiwell

CC plates are specified from the detected result; and (i) the clones are

CC reconstituted as the positions on the chromosome and arrayed. The

CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent

CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634

CC represent PCR primers for human chromosome 21q22.1, which are

CC specifically claimed for use in the present invention.

SO Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 other;

Query Match 74.3%; Score 10.4; DB 24; Length 18;

Best Local Similarity 84.6%; Pred. No. 1.3e+04;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13  
 ||||| ||||  
 Db 14 CCAGGTGACAGTCC 2

RESULT 12  
 AAA58857/C  
 ID AAA58857 standard; DNA; 19 BP.

AC AAA58857;

DT 20-OCT-2000 (first entry)



DE Oligonucleotide used for analysis and study of 2q breakpoint region.  
 XX Tissue repair protein; orofacial clefting; wound healing;  
 KW tissue repair; 2q breakpoint region; ss.  
 OS Homo sapiens.  
 XX WO200040719-A2.  
 XX 13-JUL-2000.  
 PD  
 XX  
 PF 06-JAN-2000; 2000WO-GB000003.  
 XX  
 XX 06-JAN-1999; 99GB-0000167.  
 XX  
 XX (UYLE-) UNIV LEEDS.  
 PA  
 XX Markham AF, Bonthron D;  
 PI  
 XX WPI: 2000-465983/40.  
 DR  
 XX  
 XX New human and mouse nucleic acids encoding a tissue repair protein,  
 PT useful for diagnosing and treating orofacial clefting, and for  
 PT promoting wound healing and/or tissue repair  
 XX  
 XX Disclosure: Page 44; 45pp; English.  
 PS  
 XX Oligonucleotides AA58825-58 were used in the analysis and study of  
 CC the 2q breakpoint region, in the course of the invention to identify  
 CC the gene encoding a tissue repair protein. Tissue repair gene  
 CC polynucleotides are useful for determining expression of mRNA in  
 CC selected target tissue, e.g. for diagnosing and treating orofacial  
 CC clefting. They are also useful for determining the presence  
 CC of DNA mutations in patients suffering from, or suspected to be  
 CC suffering from orofacial clefting. The antibodies are also useful  
 CC in the diagnosis of orofacial clefting. The polynucleotide is also  
 CC useful for promoting wound healing and tissue repair.  
 CC  
 XX Sequence 19 BP; 4 A; 7 C; 5 G; 3 T; 0 other:  
 SQ  
 Query Match 74.3%; Score 10.4; DB 21; Length 19;  
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CCAGGTGAGNC 13  
 DB 13 CCAGGTGAGTCC 1

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 PA (DAND) DANA FARBER CANCER INST.  
 XX  
 PI Borriello F, Freeman GJ, Nadler LM, Sharpe AH;  
 XX  
 XX WPI: 1995-320574/41.  
 DR  
 XX  
 PT Novel T cell co-stimulatory molecules - corresponding to naturally  
 PT occurring alternatively spliced forms of T cells co-stimulatory  
 PT molecules or variants  
 XX  
 XX Example 7; Page 43; 11pp; English.  
 PS  
 XX RT-PCR was used to amplify mouse T-cell costimulatory molecule  
 CC B7-1 cDNA fragments derived from murine spleen cell RNA. The  
 CC primers used for primary PCR were a sense primer (AAT01068) and  
 CC antisense primer (AAT01070), and for secondary PCR were a sense  
 CC primer (AAT01069) and antisense primer (AAT01071). cDNA fragments  
 CC were detected that encoded a B7-1 form in which the signal  
 CC peptide domain was spliced directly to the Igc-1like domain,  
 CC i.e. the Igv-1like domain was deleted (see AAR82900). Another cDNA  
 CC fragment coded for a B7-1 form in which the Igv-1like domain was  
 CC spliced directly to the transmembrane domain, i.e. the Igc-1like  
 CC domain was deleted (see AAR82902).  
 CC  
 XX Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other:  
 SQ  
 Query Match 74.3%; Score 10.4; DB 16; Length 20;  
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CCAGGTGAGNC 13  
 DB 1 CCAGGTGAGTCC 13

RESULT 14  
 AAV48029  
 ID AAV48029 standard; DNA; 20 BP.  
 XX  
 AC AAV48029;  
 XX  
 DT 19-OCT-1998 (first entry)  
 XX  
 DE Murine B7-1 targeted oligonucleotide 14914.  
 XX  
 KW ss; mouse; B7; T cell; inflammation; autoimmune disease; cell activation;  
 KW cell proliferation.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20 /\*tag= a  
 FT /note= "Phosphorothioate linkages"  
 FT  
 XX  
 PN WO9829124-A1.  
 XX  
 XX 09-JUL-1998.  
 PD  
 XX 16-DEC-1997; 97WO-US23270.  
 XX  
 PF 31-DEC-1996; 96US-0777266.  
 XX  
 PR (ISIS-) ISIS PHARM INC.  
 XX  
 PA Bennett CF, Vickers TA;  
 XX  
 XX WPI: 1998-387783/73.  
 DR  
 XX  
 PT New oligo:nucleotide(s) that modulate expression of B7 proteins -  
 PT used for, e.g. controlling activation and proliferation of T cells,

PT particularly for treatment, diagnosis and prevention of inflammation  
 XX Example 1; Page 36; 120pp; English.  
 PS  
 XX The oligonucleotides which specifically hybridise to B7 modulate its  
 CC expression (and thus T cell activation and proliferation). This is  
 CC particularly useful for treatment and prevention of inflammation and  
 CC autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,  
 CC Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,  
 CC (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,  
 CC rhinitis, allergy, cancer and metastases. The oligonucleotides may also  
 CC be used to manipulate T cell activation ex vivo; to determine or detect  
 CC B7 protein expression; for diagnosis; as assay and purification reagents,  
 CC and to study physiological roles of B7 proteins.  
 XX  
 SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 other;

Query Match 74.3%; Score 10.4; DB 19; Length 20;  
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCC 13  
 ||||| 1 11  
 Db 2 CCAGGTGAAGTCC 14

RESULT 15  
 AAA91878/c  
 ID AAA91878 standard; DNA; 20 BP.

AC AAA91878;  
 XX  
 DT 08-JAN-2001 (first entry)  
 XX

DE Antisense primer to amplify bases 66 to 265 of human TGF b1 gene.

XX TGF b1; promoter region; gene therapy; end-stage renal disease; ESRD;  
 KM human; primer; ss.  
 XX

OS Homo sapiens.

XX WO200049169-A1.

PD 24-AUG-2000.

XX 18-FEB-2000; 2000WO-US04251.

XX 19-FEB-1999; 99US-0120787.

XX (DZGE-) DZGENES LLC.

XX Moskowitz DM;

DR WPI; 2000-549279/50.

XX Diagnosing genetic susceptibility for end-stage renal disease using  
 PT single nucleotide polymorphisms, involves analyzing sample obtained  
 PT from subject to detect genetic polymorphism in the sample  
 PT polynucleotide -  
 XX

PS Example 3; Page 36; 73pp; English.

XX The present invention relates the diagnosis of genetic susceptibility  
 CC for end-stage renal disease (ESRD). The method involves analyzing a  
 CC polynucleotide sample for a single nucleotide polymorphism (SNP)  
 CC associated with an altered susceptibility for ESRD. The method allows  
 CC early detection of ESRD and hence effective delay or ideally,  
 CC prevention of ESRD is made possible. The present sequence is a primer  
 CC used to amplify bases 66 to 265 of human TGF b1 gene. Polymorphisms  
 CC the TGF b1 gene are known to be a probable trigger for renal apoptosis.  
 XX

SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 other;

Query Match 74.3%; Score 10.4; DB 21; Length 20;  
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;  
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CCAGGTGTAGNCC 13  
 ||||| 1 11  
 Db 15 CCAGGTGTAGTCC 3  
 Search completed: June 21, 2003, 22:26:27  
 Job time : 78.7812 secs

CITY: Los Angeles

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,684B  
FILING DATE: January 16, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/000,951  
FILING DATE: July 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 820:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-585-684B-820

Query Match 74.3%; Score 10.4; DB 2; Length 15;  
Best Local Similarity 84.6%; Pred. No. 1.5e+03;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAGGTGAGNCC 13  
Db 15 CCAGGTGAGTCC 3

RESULT 3  
US-08-585-684B-821/C  
Sequence 821, Application US/08585684B  
Patent No. 5877021  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,684B  
FILING DATE: January 16, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/000,951  
FILING DATE: July 7, 1995  
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 821:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-585-684B-821

Query Match 74.3%; Score 10.4; DB 2; Length 15;  
Best Local Similarity 84.6%; Pred. No. 1.5e+03;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCAGGTGAGNCC 13  
Db 14 CCAGGTGAGTCC 2

RESULT 4  
US-09-038-073-820/C  
Sequence 820, Application US/09038073  
Patent No. 6194150  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,073  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,684  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 820:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-038-073-820

Query Match 74.3%; Score 10.4; DB 4; Length 15;

Best Local Similarity 84.6%; Pred. No. 1.5e+03;  
Matches 11: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGATAGCC 13  
Db 15 CCAGGTGATAGTCC 3

## RESULT 5

US-09-038-073-821/C  
Sequence 821, Application US/09038073  
Patent No. 6194150

## GENERAL INFORMATION:

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Jarvis, Thale

APPLICANT: McSwigen, James

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

NUMBER OF SEQUENCES: 2751

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/038.073

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/585,684

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/078

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 821:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-038-073-821

Query Match

Best Local Similarity 74.3%;

Matches 11: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGATAGCC 13  
Db 14 CCAGGTGATAGTCC 2

## RESULT 6

US-09-213-719-14/C  
Sequence 14, Application US/09213719B  
Patent No. 6150162

## GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF CD44 EXPRESSION

FILE REFERENCE: RTS-0006  
CURRENT APPLICATION NUMBER: US/09/213,719B  
CURRENT FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 91

SEQ ID NO 14

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-213-719-14

Query Match

Best Local Similarity 74.3%;

Matches 11: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGGTGATAGCCA 14  
Db 16 CAGGTGATAGTCCA 4

## RESULT 7

US-08-777-266A-68  
Sequence 68, Application US/08777266A  
Patent No. 6077833

## GENERAL INFORMATION:

APPLICANT: Clarence Frank Bennett

APPLICANT: Timothy A. Vickers

TITLE OF INVENTION: Oligonucleotide Compositions and

TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Jane Massey Licata

STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill

STATE: NJ

COUNTRY: USA

ZIP: 08002

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/777,266A

FILING DATE: December 31, 1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 20

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: linear

ANTI-SENSE: Yes

US-08-777-266A-68

Query Match

Best Local Similarity 74.3%;

Matches 11: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGATAGCC 13  
Db 2 CCAGGTGATAGTCC 14

## RESULT 8

US-08-205-697A-61

; Sequence 61, Application US/08205697A

; Patent No. 6218510

; GENERAL INFORMATION:

; APPLICANT: Sharpe, Arlene H.

; APPLICANT: Borriello, Francescopaulo

; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee W.

; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules

; TITLE OF INVENTION: and Uses Therefor

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE &amp; COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/205,697A

; FILING DATE: 02-Mar-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragouras, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: BMT-120

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 61:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: oligonucleotide

US-08-205-697A-61

Query Match 74.3% Score 10.4; DB 4; Length 20;

Best Local Similarity 84.6%; Pred. No. 1.5e+03;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13

Db 1 CCAGGTGAGTCC 13

## RESULT 9

US-08-702-525-61

; Sequence 61, Application US/08702525

; Patent No. 6294660

; GENERAL INFORMATION:

; APPLICANT: Sharpe, Arlene H.

; APPLICANT: Borriello, Francescopaulo

; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee W.

; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory

; TITLE OF INVENTION: Molecules and Uses Therefor

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE &amp; COCKFIELD

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,525

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/205,697

FILING DATE: 02-Mar-1994

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: BMT-120CPUS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: oligonucleotide

US-08-702-525-61

Query Match 74.3% Score 10.4; DB 4; Length 20;

Best Local Similarity 84.6%; Pred. No. 1.5e+03;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13

Db 1 CCAGGTGAGTCC 13

## RESULT 10

US-09-326-186B-68

; Sequence 68, Application US/09326186B

; Patent No. 6319906

; GENERAL INFORMATION:

; APPLICANT: Bennett, Clarence Frank

; APPLICANT: Vickers, Timothy A.

; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the

; TITLE OF INVENTION: Modulation of the Expression of B7 Protein

; FILE REFERENCE: ISPH-0376

; CURRENT APPLICATION NUMBER: US/09/326,186B

; PRIOR FILING DATE: 1999-06-04

; PRIOR FILING DATE: 1996-12-31

; NUMBER OF SEQ ID NOS: 226

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 68

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-09-326-186B-68

Query Match 74.3% Score 10.4; DB 4; Length 20;

Best Local Similarity 84.6%; Pred. No. 1.5e+03;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13

Db 2 CCAGGTGAGTCC 14

## RESULT 11

US-09-907-843-48/C

; Sequence 48, Application US/09907843

; Patent No. 6440739

```

; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSION
; FILE REFERENCE: RTS-0279
; CURRENT APPLICATION NUMBER: US/09/907,843
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-907-843-48

```

```

Query Match          74.3%; Score 10.4; DB 4; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 CCAGGTGTAGNCCA 14
        ||||||| |||
DB      13 CAGGTGTATCCA 1

```

```

RESULT 12
PCT-US95-02576-61
; Sequence 61, Application PC/TUS9502576
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02576
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
PCT-US95-02576-61

```

```

Query Match          74.3%; Score 10.4; DB 5; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 CCAGGTGTAGNCC 13
        ||||||| |||

```

```

DB      1 CCAGGTGAGTCC 13

```

```

RESULT 13
US-07-998-289B-26/C
; Sequence 26, Application US/07998289B
; Patent No. 6027876
; GENERAL INFORMATION:
; APPLICANT: Black, Bruce C
; APPLICANT: Taylor, Martin
; APPLICANT: Heckel, David G
; TITLE OF INVENTION: Method for Monitoring Pesticide
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/998,289B
; FILING DATE: 30-Dec-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph R
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 0646/0A939
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Heliothis virescens
; IMMEDIATE SOURCE:
; CLONE: HSC 4325+
US-07-998-289B-26

```

```

Query Match          74.3%; Score 10.4; DB 3; Length 23;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 CCAGGTGTAGNCC 13
        ||||||| |||
DB      21 CCAGGTGTAGTTC 9

```

```

RESULT 14
US-08-859-998-1077
; Sequence 1077, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jekhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.

```

```

STREET: 22200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875

INFORMATION FOR SEQ ID NO: 1077:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer

US-08-859-998-1077

Query Match 74.3% Score 10.4; DB 2; Length 24;
Best Local Similarity 84.6%; Pred No.1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

QY 1 CCAGGTGTAGNCC 13
||||||| 1
Db 1 CCAGGTGTAGCTC 13

RESULT 15
US-08-765-332-4
Sequence 4, Application US/08765332
Patent No. 6025132
GENERAL INFORMATION:
APPLICANT: JANNES, GERT
APPLICANT: ROSSAU, RUDI
APPLICANT: VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIVE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,332
FILING DATE: 23-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: WO PCT/EP95/02452  
 FILING DATE: 23-JUN-1995  
 PRIOR APPLICATION DATA: EP 95870032.0  
 APPLICATION NUMBER: EP 95870032.0  
 FILING DATE: 07-APR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 94870106.5  
 FILING DATE: 24-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SADOFF, B.J.  
 REGISTRATION NUMBER: 36,663  
 REFERENCE/DOCKET NUMBER: 1487-14  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-816-4091  
 TELEFAX: 703-816-4100  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-765-332-4

Query Match	Score 10.4	DB 3	Length 24
Best Local Similarity	84.6%	Pred. No. 1.5e+03	
Matches 11; Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;
QY	1 CCAGCTGTAGMC	13	
		11	
Db	9 CCAGCTGTGTCC	21	

Search completed: June 22, 2003, 00:01:36  
Job time : 18.625 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:28:37 ; Search time 604.734 seconds  
(without alignments)  
374.936 Million cell updates/sec

Title: US-09-964-666-13

Perfect score: 14

Sequence: 1 CCAGCTGTAGNCCA 14

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estbta:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estcov:\*  
6: em\_estcpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	78.6	41	17	AL766269 Arabidops
2	10.4	74.3	37	17	AZ850196
3	10.4	74.3	37	17	BH129921
4	10.4	74.3	38	10	BE534187
5	10.4	74.3	41	10	AV832412
6	10.4	74.3	48	13	BI154032

Result No.	Score	Query Match	Length	DB ID	Description
7	10.4	74.3	49	12	BE739587
8	10	71.4	28	14	R63848
9	10	71.4	31	17	AZ346490
10	10	71.4	43	17	AZ832832
11	10	71.4	46	9	AA677571
12	9.8	70.0	28	9	AA510334
13	9.8	70.0	31	13	BI259862
14	9.8	70.0	42	17	BH791916
15	9.8	70.0	45	17	AZ579484
16	9.8	70.0	45	17	AZ445734
17	9.8	70.0	46	9	AA127131
18	9.8	70.0	48	14	C21079
19	9.8	70.0	49	14	T93720
20	9.8	70.0	50	9	AU105239
21	9.8	70.0	50	9	AU107231
22	9.8	70.0	50	13	BM182676
23	9.8	70.0	50	14	N34794
24	9.4	67.1	25	17	AZ864400
25	9.4	67.1	27	17	AZ772618
26	9.4	67.1	33	17	AZ585484
27	9.4	67.1	33	17	AL766826
28	9.4	67.1	34	17	AZ581060
29	9.4	67.1	36	17	AZ461229
30	9.4	67.1	37	17	AZ601449
31	9.4	67.1	39	17	AZ875800
32	9.4	67.1	40	9	AA991123
33	9.4	67.1	43	9	AA910920
34	9.4	67.1	43	17	AZ872071
35	9.4	67.1	47	17	AZ628215
36	9.4	67.1	49	9	AI1719563
37	9.4	67.1	49	14	T68434
38	9.4	67.1	49	17	AZ470802
39	9.4	67.1	50	9	AU104849
40	9.4	67.1	50	17	BH233070
41	9.4	67.1	50	9	AI219622
42	9.4	67.1	29	17	AZ491277
43	9.4	67.1	29	17	TA97A010
44	9.4	67.1	30	17	AZ924604
45	9.4	67.1	31	17	AZ492224

## ALIGNMENTS

RESULT 1  
AL766269/c 41 bp DNA linear GSS 18-JUN-2002  
Arabidopsis thaliana T-DNA flanking sequence GK-209A10-014557,  
genomic survey sequence.  
AL766269  
AL766269.1 GI:21519402  
GSS.  
SOURCE  
thale cress.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
1  
Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.  
and Weisshaar,B.  
A pipeline for automated high-throughput generation of FSTs  
(flanking sequence tags) from Arabidopsis thaliana T-DNA  
transformed lines  
Unpublished  
2  
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
for flanking sequence tag based reverse genetics  
Unpublished  
3 (bases 1 to 41)  
Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.  
Direct Submission  
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer

## COMMENT

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence is recovered from the left border of the T-DNA. It  
indicates an insertion within the locus defined by clone f2611.  
The sequences are generated at the MPI for Plant Breeding Research  
in the context of the GABI-Kat project. GABI-Kat is part of the  
German Plant Genomics Program designated 'GABI'. Information on  
line availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

## FEATURES

source

1. 41  
Location/Qualifiers  
/organism="Arabidopsis thaliana"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="GK-209A10-014557"  
/note="PCR was performed on DNA from Arabidopsis thaliana  
plants (T1) which were transformed with the T-DNA from  
vector pAC161. The lines contain one or more T-DNA  
insertions. The DNA fragment(s) resulting from the PCR  
were directly sequenced to determine the genomic sequence  
flanking the insertion. Sequences displaying significant  
similarity to the A. thaliana nuclear genome sequence were  
processed for submission. T-DNA derived sequences were  
removed"

BASE COUNT  
ORIGIN

8 a 12 c 9 g 12 t

Query Match 78.6%; Score 11; DB 17; Length 41;  
Best Local Similarity 91.7%; Pred. No. 3.1e+04;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 AGGTGTAGNCCA 14  
|||||

Db 30 AGGTGTAGCCCA 19

RESULT 2 37 bp DNA linear GSS 21-FEB-2001  
LOCUS A2850196  
DEFINITION 2M0151P19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0151P19 R, DNA sequence.

ACCESSION A2850196  
VERSION A2850196.1 GI:13034963  
KEYWORDS GSS.

SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 37)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beaacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0151 row: P column: 19  
Seq primer: CACACAGAAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 37.

## FEATURES

source

1. 37  
Location/Qualifiers  
/organism="Mus musculus"  
/strain="C57BL/6J"

/db\_xref="taxon:10090"  
/clone="UUGC2M0151P19"  
/clone.lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (q11473211419b1AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT  
ORIGIN

8 a 7 c 12 g 10 t

Query Match 74.3%; Score 10.4; DB 17; Length 37;  
Best Local Similarity 84.6%; Pred. No. 6.7e+04;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCC 13  
|||||

Db 23 CCAGGTGTAGCAC 35

RESULT 3 37 bp DNA linear GSS 23-JUL-2001  
LOCUS BH129921  
DEFINITION G-6c8.f Maize Random Small-insert Genomic Library Zea mays genomic  
clone G-6c8 both, DNA sequence.

ACCESSION BH129921  
VERSION BH129921.1 GI:14998762  
KEYWORDS GSS.

SOURCE Zea mays.  
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 37)  
AUTHORS Meyers,B.C., Tingey,S.V. and Morgante,M.  
TITLE Abundance, distribution and transcriptional activity of repetitive  
elements in the maize genome  
JOURNAL Genome Res. 11 (10), 1660-1676 (2001)  
MEDLINE 21475670  
COMMENT Contact: Morgante M  
Suite 200  
Dupont Genomics  
PO Box 6104, Newark, DE 19714-6104, USA  
Tel: 302 631 2638  
Fax: 302 631 2607  
Email: Michele.morgante@usa.dupont.com  
Sequences were trimmed to include only high quality bases; forward  
and reverse reads were assembled when significant overlaps were  
detected.  
Seq primer: M13univ  
Class: shotgun.

## FEATURES

source

1. 37  
Location/Qualifiers  
/organism="Zea mays"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="G-6c8"

```

/clone_lib="Maize Random Small-Insert Genomic Library"
/sex="hermaphrodite"
/tissue_type="leaf"
/cell_type="young leaf"
/dev_stage="seedling"
/note="Vector: PCR-Script; Total genomic DNA was nebulized
; ends were polished with Pfu polymerase and the fragments
cloned into PCR-Script."
BASE COUNT      6 a      12 c      11 g      4 t      4 others
ORIGIN

```

Query Match Similarity	74.3%	Score	10.4	DB	17	Length	37
Best Local Similarity	84.6%	Pred	No. 6	7e+04			
Matches	11	Conservative	0	Mismatches	2	Indels	0
						Gaps	0

QY	1	CCAGGTGTAGNCC	13
	1		11
Db	12	CCGGGTGTAGCCC	24

[illegible]

REFERENCE 1 (Pages 1 to 38)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

```

FEATURES
source
1. .38
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1M6772 row: p column: 23
High quality sequence start: 38.
Location/Qualifiers
1. .38

```

```

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="3596038"
/clone_1b="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-Sport6; Site-1: Salt
Site-2: Nott; Cloned unidirectionally. Primer: Oligo dT
library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

```

	Query Match	Score	DB	Length
	74.3%	10.4	10	38
	Best Local Similarity	84.6%		
	Pred. No. 6.7e+04			
Matches	11; Conservative	0; Mismatches	2; Indels	0; Gaps
Q7	1 CCAGGTGAGMC	13		
		11		
		11		
db	15 CCAGGTGAGGCC	27		

RESULT	5
AV832412/c	
LOCUS	AV832412.1
DEFINITION	41 bp mRNA linear EST 22-JUN-2001
ACCESSION	AV832412
VERSION	AV832412.1
KEYWORDS	GI:14524501
SOURCE	EST.
ORGANISM	Hordeum vulgare subsp. vulgare. Hordeum vulgare subsp. vulgare. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Hordeum. 1 (bases 1 to 41) Sato,K.
REFERENCE	Batley EST sequencing project in NIG and Okayama Univ
AUTHORS	Unpublished (2001)
TITLE	Contact: Kazuniro Sato
JOURNAL	
COMMENT	

Research Institute for Biosciences  
Okayama University, Barley Germplasm Center  
Chuo 2-20-1, Kurashiki, Okayama 710-0045, Japan  
Email: kazato@rib.okayama-u.ac.jp,  
URL: <http://www.rib.okayama-u.ac.jp/barley/>  
Sato, K., Saitoh, K., Takeeda, K., Shimi, T. and Kohara, Y. Direct  
submission:  
database: <http://www.shigen.nig.ac.jp/barley/Barley.html>

```

FEATURES
source
location/Qualifiers
1..41
/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Akashniriki"
/db_xref="taxon:112509"
/clone="baak12m18"
/clone_1bp="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare leaves vegetative stage"
/tissue_type="leaves"
/dev_stage="vegetative stage"
7 a 9 c 18 g 7 t
BASE COUNT
ORIGIN

```

	Query Match	Similarity	Score	DB	length
Best Local	74.3%	84.6%	10.4	10	41
Matches	11	Conservative	0	Mismatches	2
				Indels	0
				Gaps	0

RESULT 6  
B1154032/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

B1154032 48 bp mRNA linear EST 05-JUL-2001  
602887109662 NCI\_CGAP\_Mam2 Mus musculus cDNA clone IMAGE:5003014 5'  
mRNA sequence.  
B1154032  
B1154032.1 GI:14614033  
EST  
house mouse.  
Mus musculus  
Euarctota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 48)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Email: [cgabbs@email.nih.gov](mailto:cgabbs@email.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MCC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1038 row: p column: 23  
High quality sequence stop: 44.  
Location/Qualifiers

## FEATURES

source

1.48  
/organism="Mus musculus"  
/strain="FVB/N-3"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5003014"  
/clone\_lib="NCL\_CGAP\_Mam2"  
/tissue\_type="tumor, diopsy sample"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-Sport6; Site:1; Salt:  
Site:2; NotI: Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"  
BASE COUNT 9 a 10 c 23 g 6 t  
ORIGIN

Query Match 74.3%; Score 10.4; DB 13; Length 48;  
Best local Similarity 84.6%; Pred. No. 7.2e+04;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13  
1111111111  
Db 41 CCAGGAGTAGCC 29

RESULT 7  
BE739587 49 bp mRNA linear EST 15-SEP-2000  
LOCUS 6015655871 NIH\_MGC\_58 Homo sapiens CDNA clone IMAGE:3826142.3',  
DEFINITION mRNA sequence.  
ACCESSION BE739587  
VERSION BE739587.1 GI:10153579  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 49)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@pbi.nlm.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM493 row: d column: 15  
High quality sequence stop: 33  
High quality sequence stop: 49.  
Location/Qualifiers

## FEATURES

source

1.49  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3826142"  
/clone\_lib="NIH\_MGC\_58"  
/tissue\_type="hypermethroma"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: Kidney; Vector: pNR-LIB (Clontech); Site:1;  
Site:2; NotI: Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"  
BASE COUNT 9 a 10 c 23 g 6 t  
ORIGIN

insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA).  
BASE COUNT 7 a 21 c 12 g 9 t  
ORIGIN

Query Match 74.3%; Score 10.4; DB 12; Length 49;  
Best local Similarity 84.6%; Pred. No. 7.2e+04;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13  
1111111111  
Db 17 CCAGGTGTAGCC 5

RESULT 8  
R63848 28 bp mRNA linear EST 26-MAY-1995  
LOCUS Y121a09.r1 Soares placenta Nb2HP Homo sapiens CDNA clone  
DEFINITION IMAGE:139864.5' similar to SP:TSC2\_MOUSE Q00992 PUTATIVE REGULATORY  
PROTEIN ;, mRNA sequence.  
ACCESSION R63848  
VERSION R63848.1 GI:835727  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 28)  
Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkin, M., Holman  
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston  
R., Williamson, A., Woldmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: M13RP1  
High quality sequence stop: 1.  
Location/Qualifiers

## FEATURES

source

1.28  
/organism="Homo sapiens"  
/db\_xref="GDB:550462"  
/db\_xref="taxon:9606"  
/clone="IMAGE:139864"  
/clone\_lib="Soares placenta Nb2HP"  
/sex="female"  
/dev\_stage="placenta obtained at birth (full term)"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: placenta; Vector: pRT3D (Pharmacia) with a  
modified polylinker; Site:1; Not I; Site:2; Eco RI; 1st  
strand CDNA was primed with a Not I - oligo(dT) primer [5'  
ACTGGAAGATTCGCGCCGAGAGATTTTCTTTTCTTTTCTTTT 3']  
double-stranded CDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pRT3D vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo.  
BASE COUNT 8 a 6 c 8 g 6 t  
ORIGIN

Query Match 71.4%; Score 10; DB 14; Length 28;  
Best Local Similarity 90.9%; Pred. No. 1e+05;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GGCTAGNCCA 14  
1111111111  
Db 12 GGCTAGACCA 22

## RESULT 9

AZ346490 31 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0081004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0081004 R. DNA sequence.

ACCESSION

AZ346490

VERSION

A2346490.1

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0081 row: 0 column: 04  
Seq primer: CACACAGGAACACGATGACG  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers  
1. 31  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0081004"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adapter oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g114732114g1A129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## FEATURES

source

1. 31

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0081004"

/clone\_1lb="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adapter oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g114732114g1A129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT

ORIGIN

7 a 11 c 5 g 8 t

Query Match 71.4%; Score 10; DB 17; Length 31;  
Best Local Similarity 90.9%; Pred. No. 1.1e+05;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CAGGTAGNCC 12  
1111111111  
Db 23 CAGGTAGTGC 13

## RESULT 10

A2832832 43 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0113D06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0113D06 R. DNA sequence.

ACCESSION

A2832832

VERSION

A2832832.1

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 43)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.  
and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0113 row: 0 column: 06  
Seq primer: CACACAGGAACACGATGACG  
Class: plasmid ends  
High quality sequence stop: 43.  
Location/Qualifiers  
1. 43  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0113D06"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adapter oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g114732114g1A129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## FEATURES

source

1. 43

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0113D06"

/clone\_1lb="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adapter oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g114732114g1A129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

BASE COUNT

ORIGIN

15 a 9 c 11 g 8 t



ACCESSION mRNA sequence.  
 B1259862  
 VERSION B1259862.1 GI:14817604  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 31)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: ARCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: Incyte Genomics, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov  
 plate: L1AM1269 row: 0 column: 05  
 high quality sequence stop: 31.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:5111260"  
 /clone\_1lb="NIH-MGC\_12"  
 /tissue\_type="cervical carcinoma cell line"  
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NOTI; Site: 2; SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.4 kb. Library prepared by Life Technologies."  
 3 a 12 c 6 g 10 t

BASE COUNT  
 ORIGIN

Query Match 70.0%; Score 9.8; DB 13; Length 31;  
 Best Local Similarity 78.6%; Pred. No. 1.4e+05;  
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCCA 14  
 11111 11111  
 23 CCAGGAGAGGCCA 10

Db

RESULT 14  
 BH791916 42 bp DNA linear GSS 02-APR-2002  
 LOCUS SALK\_061994.25.20 x Arabidopsis thaliana TDNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_061994.25.20.x, DNA sequence.  
 ACCESSION BH791916  
 VERSION BH791916.1 GI:19886386  
 KEYWORDS GSS.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 1 (bases 1 to 42)  
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadri nab  
 , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Predits,L., Shinn,P.  
 , Zimmerman,J. and Ecker,J.R.  
 A Sequence-Indexed Library of Insertion Mutations in the  
 Arabidopsis Genome  
 Unpublished (2001)  
 Contact: Joseph R. Ecker  
 Salk Institute Genomic Analysis Laboratory (SIGAL)  
 The Salk Institute for Biological Studies  
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
 Tel: 858 453 4100 x1752

JOURNAL  
 COMMENT

Fax: 858 558 6379  
 Email: eckersalk.edu  
 This is single pass sequence recovered from the left border of  
 TDNA. This sequence lies within 300 bases of the 5' end of  
 At2g29210.  
 Class: TDNA tagged.  
 Location/Qualifiers  
 1. 42  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="SALK\_061994.25.20.x"  
 /clone\_1lb="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines  
 each of which contains one or more TDNA insertion  
 elements. The resultant fragment for each line was  
 directly sequenced to determine the genomic sequence at  
 the site of insertion. Details of the protocols used can  
 be found at http://signal.salk.edu/tdna\_protocols.html"

BASE COUNT 11 a 11 c 6 g 14 t

ORIGIN

Query Match 70.0%; Score 9.8; DB 17; Length 42;  
 Best Local Similarity 78.6%; Pred. No. 1.5e+05;  
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCCA 14  
 11111 11111  
 8 CCAGTTTACGCCA 21

Db

RESULT 15  
 A2579484 44 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0367B06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION A2579484  
 ACCESSION A2579484  
 VERSION A2579484.1 GI:11693913  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 44)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
 , M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhauser,A.  
 and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SUC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0367 row: B column: 06  
 Seq primer: CGTTGTAACGACGCGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 44.  
 Location/Qualifiers  
 1. 44  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
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 /clone="UUGC1M0367B06"  
 /clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

JOURNAL  
 COMMENT

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 11 c 13 g 11 t  
ORIGIN

Query Match 70.0%; Score 9.8; DB 17; Length 44;  
Best Local Similarity 78.6%; Pred. No. 1.5e+05;  
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGTGTAGNCCA 14  
|||||  
Db 18 CCAGATGTAGACGA 5

Search completed: June 21, 2003, 23:59:07  
Job time : 610.901 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 281.094 Seconds

(without alignments)  
1449.478 Million cell updates/sec

Title: US-09-964-666-14

Perfect score: 14

Sequence: 1 CAAGTCGAGNCCA 14

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_cm:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_or:\*

21: em\_ov:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_in:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rnd:\*

36: em\_htg\_man:\*

37: em\_htg\_vit:\*

38: em\_sy:\*

39: em\_htg\_hum:\*

40: em\_htg\_mus:\*

41: em\_htg\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12	85.7	24	6	AX443826
C 2	12	85.7	25	6	AX447806
C 3	11.4	81.4	17	6	AR006801
C 4	11.4	81.4	17	6	AR008981
C 5	11.4	81.4	17	6	AR135409
C 6	11.4	81.4	17	6	161180
C 7	11.4	81.4	17	6	171313
C 8	11.4	81.4	17	6	178729
C 9	11.4	81.4	18	6	AX250348
C 10	11.4	81.4	22	6	AR103422
C 11	11.4	81.4	22	6	AR151630
C 12	11.4	81.4	24	6	AX350160
C 13	11.4	81.4	26	6	AR006770
C 14	11.4	81.4	26	6	AR135378
C 15	11.4	81.4	26	6	171282
C 16	11.4	81.4	27	6	A40952
C 17	11.4	81.4	27	6	A44325
C 18	11.4	81.4	27	6	A80258
C 19	11.4	81.4	27	6	AR076531
C 20	11.4	81.4	27	6	E38897
C 21	11.4	81.4	29	6	BD013342
C 22	11.4	81.4	29	23	BD010299
C 23	11.4	81.4	30	6	AR067963
C 24	11.4	81.4	30	6	AR078918
C 25	11.4	81.4	30	6	AR097712
C 26	11.4	81.4	32	6	E10691
C 27	11.4	81.4	34	6	E40701
C 28	11.4	81.4	38	6	AR096917
C 29	11.4	81.4	38	6	AX467501
C 30	11.4	81.4	38	6	112040
C 31	11.4	81.4	39	6	AX374843
C 32	11.4	81.4	39	6	AX467500
C 33	11.4	81.4	46	6	AR035242
C 34	11	78.6	23	6	AX306373
C 35	11	78.6	23	6	AX320086
C 36	11	78.6	23	6	AX352397
C 37	11	78.6	23	6	AX419617
C 38	10.6	75.7	21	6	AX095382
C 39	10.6	75.7	31	6	AX249084
C 40	10.4	74.3	15	6	AR180271
C 41	10.4	74.3	19	6	AX131418
C 42	10.4	74.3	20	6	AX296985
C 43	10.4	74.3	20	6	AX370507
C 44	10.4	74.3	20	6	E35314
C 45	10.4	74.3	20	6	E35315

# ALIGNMENTS

RESULT 1

AX443826/c

LOCUS AX443826 24 bp DNA

DEFINITION Sequence 281 from Patent WO0216649.

ACCESSION AX443826

VERSION AX443826.1 GI:21691104

KEYWORDS

SOURCE

ORGANISM

synthetic construct.

synthetic construct

artificial sequences.

REFERENCE

1 Gunderson, K.

AUTHORS

Probes and decoder oligonucleotides

TITLE Patent: WO 0216649-A 281 28-FEB-2002;

JOURNAL Illumina, Inc. (US)

FEATURES Location/Qualifiers  
source 1..24  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Computer Generated Probe Sequence."  
BASE COUNT 5 a 5 c 8 g 6 t  
ORIGIN

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Best Local Similarity 92.3%: Pred. No. 2.5e+04;  
Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCC 13  
Db 19 CAAGTCCAGACC 7

RESULT 2  
AX447806/c AX447806 25 bp DNA Linear PAT 03-JUL-2002  
LOCUS Sequence 4261 from Patent W00216649.  
DEFINITION AX447806  
ACCESSION AX447806  
VERSION AX447806.1 GI:21696705  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Gunderson, K.  
TITLE Probes and decoder oligonucleotides  
JOURNAL Patent: WO 0216649-A 4261 28-FEB-2002;  
Illumina, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..25  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Computer Generated Probe Sequence."

BASE COUNT 5 a 5 c 8 g 7 t  
ORIGIN

Query Match 85.7%: Score 12; DB 6; Length 25;  
Best Local Similarity 92.3%: Pred. No. 2.5e+04;  
Matches 12: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCC 13  
Db 20 CAAGTCCAGACC 8

RESULT 3  
AR006801/c AR006801 17 bp DNA Linear PAT 04-DEC-1998  
LOCUS Sequence 51 from patent US 5750105.  
DEFINITION AR006801  
ACCESSION AR006801  
VERSION AR006801.1 GI:3966285  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Newman, R.A., Hanna, N. and Raab, R.W.  
TITLE Recombinant antibodies for human therapy  
JOURNAL Patent: US 5750105-A 51 12-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
BASE COUNT 3 a 5 c 6 g 3 t  
ORIGIN

Query Match 81.4%: Score 11.4; DB 6; Length 17;  
Best Local Similarity 85.7%: Pred. No. 5.8e+04;  
Matches 12: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
Db 17 CCAGTCCAGTCCA 4

RESULT 4  
AR008981/c AR008981 17 bp DNA Linear PAT 04-DEC-1998  
LOCUS Sequence 1 from patent US 5756096.  
DEFINITION AR008981  
ACCESSION AR008981  
VERSION AR008981.1 GI:3967786  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Newman, R.A., Hanna, N. and Raab, R.W.  
TITLE Recombinant antibodies for human therapy  
JOURNAL Patent: US 5756096-A 1 26-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
BASE COUNT 3 a 5 c 6 g 3 t  
ORIGIN

Query Match 81.4%: Score 11.4; DB 6; Length 17;  
Best Local Similarity 85.7%: Pred. No. 5.8e+04;  
Matches 12: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
Db 17 CCAGTCCAGTCCA 4

RESULT 6  
I61180/c I61180 17 bp DNA Linear PAT 07-OCT-1997  
LOCUS Sequence 5 from patent US 5658570.  
DEFINITION I61180  
ACCESSION I61180  
VERSION I61180.1 GI:2479128  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Hanna, N., Newman, R. Anthony, and Reff, M. Elliot.  
TITLE Recombinant anti-CD4 antibodies for human therapy  
JOURNAL Patent: US 6136310-A 44 24-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
BASE COUNT 3 a 5 c 6 g 3 t  
ORIGIN

Query Match 81.4%: Score 11.4; DB 6; Length 17;  
Best Local Similarity 85.7%: Pred. No. 5.8e+04;  
Matches 12: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 17)  
AUTHORS Newman, R.A., Hanna, N. and Raab, R.W.  
TITLE Recombinant antibodies for human therapy  
JOURNAL Patent: US 5658570-A 5 19-AUG-1997;  
FEATURES Location/Qualifiers  
source 1..17  
BASE COUNT 3 a 5 c 6 g 3 t  
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Best Local Similarity 85.7%; Pred. No. 5.8e+04;  
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QY 1 CAAGTCCAGNCCA 14  
Db 17 CCAGTCCAGTCCA 4  
RESULT 7  
LOCUS I71313 17 bp DNA linear PAT 03-APR-1998  
DEFINITION Sequence 51 from patent US 5681722.  
ACCESSION I71313  
VERSION I71313.1 GI:3007448  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Newman, R.A., Hanna, N. and Raab, R.W.  
TITLE Recombinant antibodies for human therapy  
JOURNAL Patent: US 5681722-A 51 28-OCT-1997;  
FEATURES Location/Qualifiers  
source 1..17  
BASE COUNT 3 a 5 c 6 g 3 t  
ORIGIN  
Query Match 81.4%; Score 11.4; DB 6; Length 17;  
Best Local Similarity 85.7%; Pred. No. 5.8e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CAAGTCCAGNCCA 14  
Db 17 CCAGTCCAGTCCA 4  
RESULT 8  
LOCUS I78729 17 bp DNA linear PAT 03-APR-1998  
DEFINITION Sequence 5 from patent US 5693780.  
ACCESSION I78729  
VERSION I78729.1 GI:3014883  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Newman, R.A., Hanna, N. and Raab, R.W.  
TITLE Recombinant antibodies for human therapy  
JOURNAL Patent: US 5693780-A 5 02-DEC-1997;  
FEATURES Location/Qualifiers  
source 1..17  
BASE COUNT 3 a 5 c 6 g 3 t  
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Query Match 81.4%; Score 11.4; DB 6; Length 17;  
Best Local Similarity 85.7%; Pred. No. 5.8e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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Db 17 CCAGTCCAGTCCA 4  
RESULT 9  
LOCUS AX250348/c 18 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 16 from Patent WO0168682.  
ACCESSION AX250348  
VERSION AX250348.1 GI:15984115  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Reim, S.J. and Turpen, T.H.  
TITLE Self antigen vaccines for treating b cell lymphomas and other cancers  
JOURNAL Patent: WO 0168682-A 16 20-SEP-2001;  
FEATURES Large Scale Biology Corporation (US)  
source Location/Qualifiers  
1..18  
/organism="unidentified"  
/db\_xref="taxon:32644"  
/note="primer"  
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Best Local Similarity 85.7%; Pred. No. 5.8e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CAAGTCCAGNCCA 14  
Db 15 CCAGTCCAGTCCA 2  
RESULT 10  
LOCUS AR103422 22 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 13 from patent US 6087473.  
ACCESSION AR103422  
VERSION AR103422.1 GI:12815010  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Konklin, D.C., Foster, D.C. and Gao, Z.  
TITLE Kunitz domain polypeptide and materials and methods for making it  
JOURNAL Patent: US 6087473-A 13 11-JUL-2000;  
FEATURES Location/Qualifiers  
source 1..22  
BASE COUNT 6 a 7 c 7 g 2 t  
ORIGIN  
Query Match 81.4%; Score 11.4; DB 6; Length 22;  
Best Local Similarity 85.7%; Pred. No. 5.7e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CAAGTCCAGNCCA 14  
Db 5 CAAGTCCAGAGCA 18  
RESULT 11  
LOCUS AR151630 22 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 13 from patent US 6232098.  
ACCESSION AR151630  
VERSION AR151630.1 GI:15117680  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Konklin,D.C., Foster,D.C. and Gao,Z.  
TITLE Kunitz domain polypeptide and materials and methods for making it  
JOURNAL Patent: US 6232098-A 13 15-MAY-2001;  
FEATURES Location/Qualifiers  
source 1..22  
BASE COUNT 6 a 7 c 7 g 2 t  
ORIGIN  
Query Match 81.4%; Score 11.4; DB 6; Length 22;  
Best Local Similarity 85.7%; Pred. No. 5.7e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 CAAGGTCAGNCCA 14  
DB 5 CAAGGTCAGAGCA 18  
RESULT 12  
AX350160/c AX350160 24 bp DNA linear PAT 06-FEB-2002  
LOCUS Sequence 19 from Patent WO0202775.  
DEFINITION AX350160  
ACCESSION AX350160  
VERSION AX350160.1 GI:18615834  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Boehm,T. and Dear,N.T.  
TITLE Calpain protease 12  
JOURNAL Patent: WO 0202775-A 19 10-JAN-2002;  
FEATURES BASF AKTENGESSELSCHAFT (CE)  
Location/Qualifiers  
source 1..24  
BASE COUNT 3 a 7 c 9 g 5 t  
ORIGIN  
Query Match 81.4%; Score 11.4; DB 6; Length 24;  
Best Local Similarity 85.7%; Pred. No. 5.7e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 CAAGGTCAGNCCA 14  
DB 23 CAAGGCCAGGTCCA 10  
RESULT 13  
AR006770/c AR006770 26 bp DNA linear PAT 04-DEC-1998  
LOCUS Sequence 20 from patent US 5750105.  
DEFINITION AR006770  
ACCESSION AR006770  
VERSION AR006770.1 GI:3966254  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Newman,R.A., Hanna,N. and Raab,R.W.  
TITLE Recombinant antibodies for human therapy  
JOURNAL Patent: US 5750105-A 20 12-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..26  
BASE COUNT 7 a 6 c 8 g 5 t  
ORIGIN

Query Match 81.4%; Score 11.4; DB 6; Length 26;  
Best Local Similarity 85.7%; Pred. No. 5.7e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 CAAGGTCAGNCCA 14  
DB 26 CCAGGTCAGGTCCA 13  
RESULT 14  
AR135378/c AR135378 26 bp DNA linear PAT 16-JUN-2001  
LOCUS Sequence 13 from patent US 6136310.  
DEFINITION AR135378  
ACCESSION AR135378  
VERSION AR135378.1 GI:14476050  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Hanna,N., Newman,R.Anthony. and Refi,M.Elliott.  
TITLE Recombinant anti-CD4 antibodies for human therapy  
JOURNAL Patent: US 6136310-A 13 24-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..26  
BASE COUNT 7 a 6 c 8 g 5 t  
ORIGIN  
Query Match 81.4%; Score 11.4; DB 6; Length 26;  
Best Local Similarity 85.7%; Pred. No. 5.7e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 CAAGGTCAGNCCA 14  
DB 26 CCAGGTCAGGTCCA 13  
RESULT 15  
I71282/c I71282 26 bp DNA linear PAT 03-APR-1998  
LOCUS Sequence 20 from patent US 5681722.  
DEFINITION I71282  
ACCESSION I71282  
VERSION I71282.1 GI:3007417  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Newman,R.A., Hanna,N. and Raab,R.W.  
TITLE Recombinant antibodies for human therapy  
JOURNAL Patent: US 5681722-A 20 28-OCT-1997;  
FEATURES Location/Qualifiers  
source 1..26  
BASE COUNT 7 a 6 c 8 g 5 t  
ORIGIN  
Query Match 81.4%; Score 11.4; DB 6; Length 26;  
Best Local Similarity 85.7%; Pred. No. 5.7e+04;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 1 CAAGGTCAGNCCA 14  
DB 26 CCAGGTCAGGTCCA 13  
Search completed: June 21, 2003, 22:14:42  
Job time : 284.094 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:51 ; Search time 76.7812 Seconds  
(without alignments)  
410.621 Million cell updates/sec

Title: US-09-964-666-14  
Perfect score: 14  
Sequence: 1 CAAGGTCCAGNCCA 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_101002:\*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12	85.7	24	ABQ00274	Oligonucleotide ad
C 2	12	85.7	24	ABQ04512	Oligonucleotide ad
C 3	12	85.7	24	ABQ04553	Oligonucleotide ad
C 4	12	85.7	24	ABQ10840	Oligonucleotide ad
C 5	12	85.7	24	ABQ10881	Oligonucleotide ad
C 6	12	85.7	25	ABQ12376	Oligonucleotide ad
C 7	12	85.7	25	ABQ12417	Oligonucleotide ad
C 8	11.4	81.4	17	AAQ35925	Human/monkey heavy
C 9	11.4	81.4	18	AAQ95155	Human or monkey Ig

C 10	11.4	81.4	17	AAQ91566	Cynomolgus monkey
C 11	11.4	81.4	17	AAQ62902	VH1 heavy chain va
C 12	11.4	81.4	17	AAV31430	Cynomolgus immunog
C 13	11.4	81.4	17	AAV23793	Primer for Anti-CD
C 14	11.4	81.4	17	AAV05683	Human/monkey heavy
C 15	11.4	81.4	18	AAV43427	VH1 Family Specific
C 16	11.4	81.4	18	AAQ45544	Tumour-specific Ig
C 17	11.4	81.4	18	AAQ24764	5' PCR primer used
C 18	11.4	81.4	20	AAQ64442	Mouse ada gene re
C 19	11.4	81.4	20	AAQ12663	Human BAX RT-PCR p
C 20	11.4	81.4	20	AAQ99913	Primer used to amp
C 21	11.4	81.4	22	AAQ50117	Human serine prote
C 22	11.4	81.4	22	AAQ46336	Human zkus5 Kunitz
C 23	11.4	81.4	22	AAQ14335	Human zkus5 DNA am
C 24	11.4	81.4	22	ABQ55000	Human lymphoma-spe
C 25	11.4	81.4	22	ABQ99782	Human capn5 Set 1
C 26	11.4	81.4	25	AAQ75424	Primer for human a
C 27	11.4	81.4	26	AAQ35905	Human/monkey heavy
C 28	11.4	81.4	26	AAQ95124	Human or monkey Ig
C 29	11.4	81.4	26	AAQ92201	Monkey/human heavy
C 30	11.4	81.4	26	AAQ62871	Human or monkey VH
C 31	11.4	81.4	26	AAQ31384	Human or monkey he
C 32	11.4	81.4	26	AAQ23762	Primer for Anti-CD
C 33	11.4	81.4	26	AAQ05652	Human/monkey VH e
C 34	11.4	81.4	27	AAQ87238	Primer for leader
C 35	11.4	81.4	27	AAQ92804	Primer H51 for hum
C 36	11.4	81.4	27	AAQ52801	PCR primer H51 fro
C 37	11.4	81.4	27	AAQ09964	Primer H51 for hum
C 38	11.4	81.4	29	AAQ47905	IgE antibody L cha
C 39	11.4	81.4	30	AAQ67195	Humanized 130BF VH
C 40	11.4	81.4	30	AAQ56586	Heavy chain primer
C 41	11.4	81.4	30	AAQ16179	Humanised antibody
C 42	11.4	81.4	30	AAQ33320	Anti-CD23 6G5 anti
C 43	11.4	81.4	32	AAQ18053	Sense primer #1 am
C 44	11.4	81.4	34	AAQ61365	Human Immunoglobul
C 45	11.4	81.4	34	AAQ78273	Human Ig H chain s

## ALIGNMENTS

RESULT 1	ABQ00274/c	ABQ00274 standard; DNA; 24 BP.
ID	ABQ00274:	
AC	ABQ00274:	
XX		
DT	11-JUN-2002 (first entry)	
XX		
DE	Oligonucleotide adapter/capture probe 265.	
XX		
KW	Oligonucleotide array; adapter sequence; probe; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200216649-A2.	
XX		
PD	28-FEB-2002.	
XX		
PF	27-AUG-2001: 2001WO-0526519.	
XX		
PR	25-AUG-2000: 2000US-227948P.	
PR	29-AUG-2000: 2000US-228854P.	
XX		
PA	(ILLU-) ILLUMINA INC.	
XX		
PI	Gunderson K:	
XX		
DR	WPI: 2002-292068/33.	
XX		
PT	Array comprising adapter sequences useful for immobilizing or detecting	
PT	a target nucleic acid sequence, has different addresses comprising	
PT	different specific capture probes	

xx Claim 1; Page 50; 261pp; English.

xx

PS The invention relates to an oligonucleotide array (I) comprising at least

CC 25 different addresses (adapter sequences) with each comprising a

CC different capture probe selected from a group consisting of the sequences

CC given in ABO00010-ABQ13409. (I) is useful for immobilising a target

CC nucleic acid sequence by attaching a adapter nucleic acid

CC (ABO00010-ABQ13409) to a target nucleic acid to form a modified target

CC nucleic acid and contacting the modified target nucleic acid with (I).

CC The steps of above method is useful for detecting a target nucleic acid,

CC which further comprises detecting the presence of the modified target

CC nucleic acid.

CC

SQ Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;

OY Query Match 85.7%; Score 12; DB 24; Length 24;  
Best Local Similarity 92.3%; Pred. NO. 2.le+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

Db 1 CAAGGTCACAGNC 13  
||||||| ||  
19 CAAGSTCCAGACC 7

RESULT 2

ABQ04512/C  
ID ABQ04512 standard; DNA; 24 BP.

XX AC ABQ04512;  
XX DT 11-JUN-2002 (first entry)  
DE Oligonucleotide adapter/capture probe 4503.  
DE Oligonucleotide adapter; adapter sequence; probe; ss.  
KM  
KK  
XX Synthetic.  
OS WO200216649-A2.  
PN  
PM  
PD 28-FEB-2002.  
PD 27-AUG-2001; 2001WO-US26519.  
PF 25-AUG-2000; 2000US-227948P.  
PR 29-AUG-2000; 2000US-228854P.  
PX (ILLU-) ILLUMINA INC.  
PA  
XX  
XX Gunderson K;  
PI WPI; 2002-292068/33.  
DE  
PT Array comprising adapter sequences useful for immobilizing or detecting  
PT a target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes -  
XX  
XX  
PS Claim 1; Page 145; 261pp; English.

xx The invention relates to an oligonucleotide array (I) comprising at least

CC 25 different addresses (adapter sequences) with each comprising a

CC different capture probe selected from a group consisting of the sequences

CC given in ABO00010-ABQ13409. (I) is useful for immobilising a target

CC nucleic acid sequence by attaching a adapter nucleic acid

CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target

CC nucleic acid and contacting the modified target nucleic acid with (I).

CC The steps of above method is useful for detecting a target nucleic acid,

CC which further comprises detecting the presence of the modified target

CC nucleic acid.

CC

SQ Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;

Query Match	85.7%:	Score 12:	DB 24:	Length 24:
Best Local Similarity	92.3%:	Pred. No. 2.1e+03:		
Matches 12: Conservative	0:	Mismatches 1:	Indels 0:	Gaps 0:
OY	1 CAAGGTCAGNCC 13			
DB	19 CAAGGTCAGACC 7			
RESULT 3				
ID	ABO04553 standard; DNA: 24 BP.			
XX	ABO04553:			
AC	ABO04553:			
XX				
DT	11-JUN-2002 (first entry)			
XX				
DE	Oligonucleotide adapter/capture probe 4544.			
XX				
KM	Oligonucleotide array; adapter sequence; probe; ss.			
XX				
OS	Synthetic.			
XX				
PN	WO200216649-A2.			
XX				
PD	28-FEB-2002.			
XX				
PF	27-AUG-2001; 2001WO-US26519.			
XX				
PR	25-AUG-2000; 2000US-227948P.			
PR	29-AUG-2000; 2000US-228854P.			
XX				
PA	(ILLU-) ILLUMINA INC.			
XX				
PI	Gunderson K;			
DR	WPI: 2002-292068/33.			
XX				
PT	Array comprising adapter sequences useful for immobilizing or detecting			
PR	a target nucleic acid sequence, has different addresses comprising			
XX	different specific capture probes			
PS	Claim 1; Page 145; 261pp; English.			
XX				
CC	The invention relates to an oligonucleotide array (I) comprising at least			
CC	25 different addresses (adapter sequences) with each comprising a			
CC	different capture probe selected from a group consisting of the sequences			
CC	given in ABO00010-ABO13409. (I) is useful for immobilising a target			
CC	nucleic acid sequence by attaching a adapter nucleic acid			
CC	(ABO0010-ABO13409) to a target nucleic acid to form a modified target			
CC	nucleic acid and contacting the modified target nucleic acid with (I).			
CC	The steps of above method is useful for detecting a target nucleic acid,			
CC	which further comprises detecting the presence of the modified target			
CC	nucleic acid.			
XX				
SO	Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 other;			
XX				
Query Match	85.7%:	Score 12:	DB 24:	Length 24:
Best Local Similarity	92.3%:	Pred. No. 2.1e+03:		
Matches 12: Conservative	0:	Mismatches 1:	Indels 0:	Gaps 0:
OY	1 CAAGGTCAGNCC 13			
DB	6 CAAGGTCAGACC 18			
RESULT 4				
ABO10840/c				
ID	ABO10840 standard; DNA: 24 BP.			
XX				
AC	ABO10840:			
XX				
DT	11-JUN-2002 (first entry)			

XX Oligonucleotide adapter/capture probe 10831.  
DE Oligonucleotide array; adapter sequence; probe; ss.  
XX Synthetic.  
OS  
XX WO200216649-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 27-AUG-2001; 2001WO-US26519.  
XX  
XX 25-AUG-2000; 2000US-227948P.  
PR 29-AUG-2000; 2000US-228854P.  
XX  
XX (ILLU-) ILLUMINA INC.  
PA  
XX Gunderson K;  
XX  
XX WPI; 2002-292068/33.  
DR  
XX Array comprising adapter sequences useful for immobilizing or detecting  
PT a target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes  
PS Claim 1; Page 223; 261pp; English.  
XX  
XX The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching an adapter nucleic acid  
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target  
CC nucleic acid and contacting the modified target nucleic acid with (I).  
CC The steps of above method is useful for detecting a target nucleic acid,  
CC which further comprises detecting the presence of the modified target  
CC nucleic acid.  
XX  
XX Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;  
SQ  
Query Match 85.7%; Score 12; DB 24; Length 24;  
Best Local Similarity 92.3%; Pred. No. 2.1e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAAGTCCAGNCC 13  
DB 19 CAAGTCCAGACC 7  
RESULT 5  
ABQ10881  
ID ABQ10881 standard; DNA; 24 BP.  
XX  
XX ABQ10881;  
AC  
XX  
XX 11-JUN-2002 (first entry)  
DT  
XX Oligonucleotide adapter/capture probe 10872.  
DE  
XX Oligonucleotide array; adapter sequence; probe; ss.  
XX  
XX Synthetic.  
OS  
XX WO200216649-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 27-AUG-2001; 2001WO-US26519.  
PF  
XX 25-AUG-2000; 2000US-227948P.  
PR 29-AUG-2000; 2000US-228854P.  
XX  
XX

PA (ILLU-) ILLUMINA INC.  
XX  
XX Gunderson K;  
PI  
XX  
XX WPI; 2002-292068/33.  
DR  
XX  
XX Array comprising adapter sequences useful for immobilizing or detecting  
PT a target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes  
PS Claim 1; Page 223; 261pp; English.  
XX  
XX The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target  
CC nucleic acid sequence by attaching an adapter nucleic acid  
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target  
CC nucleic acid and contacting the modified target nucleic acid with (I).  
CC The steps of above method is useful for detecting a target nucleic acid,  
CC which further comprises detecting the presence of the modified target  
CC nucleic acid.  
XX  
XX Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 other;  
SQ  
Query Match 85.7%; Score 12; DB 24; Length 24;  
Best Local Similarity 92.3%; Pred. No. 2.1e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAAGTCCAGNCC 13  
DB 6 CAAGTCCAGACC 18  
RESULT 6  
ABQ12376/C  
ID ABQ12376 standard; DNA; 25 BP.  
XX  
XX ABQ12376;  
AC  
XX  
XX 11-JUN-2002 (first entry)  
DT  
XX Oligonucleotide adapter/capture probe 12367.  
DE  
XX Oligonucleotide array; adapter sequence; probe; ss.  
XX  
XX Synthetic.  
OS  
XX WO200216649-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 27-AUG-2001; 2001WO-US26519.  
PF  
XX 25-AUG-2000; 2000US-227948P.  
PR 29-AUG-2000; 2000US-228854P.  
XX  
XX (ILLU-) ILLUMINA INC.  
PA  
XX Gunderson K;  
XX  
XX WPI; 2002-292068/33.  
DR  
XX  
XX Array comprising adapter sequences useful for immobilizing or detecting  
PT a target nucleic acid sequence, has different addresses comprising  
PT different specific capture probes  
PS Claim 1; Page 242; 261pp; English.  
XX  
XX The invention relates to an oligonucleotide array (I) comprising at least  
CC 25 different addresses (adapter sequences) with each comprising a  
CC different capture probe selected from a group consisting of the sequences  
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target

CC nucleic acid sequence by attaching a adapter nucleic acid  
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target  
CC nucleic acid and contacting the modified target nucleic acid with (1).  
CC The steps of above method is useful for detecting a target nucleic acid,  
CC which further comprises detecting the presence of the modified target  
CC nucleic acid.

XX Sequence 25 BP: 5 A; 5 C; 8 G; 7 T; 0 other;

QY Query Match 85.7%; Score 12; DB 24; Length 25;

Best Local Similarity 92.3%; Pred. No. 2.1e+03; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 CAAGGTCCAGNCC 13  
20 CAAGGTCCAGACC 8

RESULT 7

ABQ12417 standard; DNA; 25 BP.

ABQ12417;

11-JUN-2002 (first entry);

Oligonucleotide adapter/capture probe 12408.

Oligonucleotide array; adapter sequence; probe; ss.

Synthetic.

WO200216649-A2.

28-FEB-2002.

27-AUG-2001; 2001WO-US26519.

25-AUG-2000; 2000US-227948P.

29-AUG-2000; 2000US-228854P.

(ILLU-) ILLUMINA INC.

Gunderson K;

WPI; 2002-292068/33.

Array comprising adapter sequences useful for immobilizing or detecting

a target nucleic acid sequence, has different addresses comprising

different specific capture probes

Claim 1; Page 242; 261pp; English.

The invention relates to an oligonucleotide array (I) comprising at least

25 different addresses (adapter sequences) with each comprising a

different capture probe selected from a group consisting of the sequences

given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target

nucleic acid sequence by attaching a adapter nucleic acid

(ABQ00010-ABQ13409) to a target nucleic acid to form a modified target

nucleic acid and contacting the modified target nucleic acid with (1).

The steps of above method is useful for detecting a target nucleic acid,

which further comprises detecting the presence of the modified target

nucleic acid.

RESULT 8  
AAQ35925/C  
ID AAQ35925 standard; DNA; 17 BP.

AAQ35925;

08-JUN-1993 (first entry)

Human/monkey heavy chain variable region primer VH1.

Amplify: polymerase chain reaction; heavy; light; chain: variable; Ig;

PCR: primer: region; lambda: human; constant; antigen: recombinant;

antibody; chimpanzee; Ag; Old world monkey; eczema; immunoglobulin;

therapeutic; rheumatoid arthritis; P-Bluescript; ss.

Synthetic.

WO9302108-A.

04-FEB-1993.

24-JUL-1992; 92WO-US06194.

25-JUL-1991; 91US-0735064.

23-MAR-1992; 92US-0856281.

(IDEC-) IDEC PHARM CORP.

Hanna N, Newman RA, Raab RW;

WPI; 1993-058729/07.

Recombinant antibodies including Old World monkey portion and

human portion - used for treatment of auto-immune diseases,

infectious diseases, AIDS, tumours, diabetes, proliferative

diseases, intestinal inflammations and allergies, etc.

Disclosure; Fig 8a; 92pp; English.

The sequences given in AAQ35925-30 represent sense primers which were

used to amplify cynomolgus heavy chain variable region sequences.

The amplified sequences belonged to a number of different gene

families. The amplified sequences were cloned into p-Bluescript

for sequencing. The amplified sequences could be used in the

production of a recombinant antibody, comprising a human, chimpanzee

or Old world monkey immunoglobulin (Ig) constant region and an antigen

(Ag) binding portion of an old world monkey Ig variable region, where

the old world monkeys may be the same or different. The recombinant

antibody may be used as a therapeutic agent for the treatment of

rheumatoid arthritis, eczema and immunological disorders.

Sequence 17 BP: 3 A; 5 C; 6 G; 3 T; 0 other;

QY Query Match 81.4%; Score 11.4; DB 14; Length 17;

Best Local Similarity 85.7%; Pred. No. 4.6e+03; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 1 CAAGTCCAGNCCA 14  
17 CCAGTCCAGTCCA 4

RESULT 9

AAAT95155/C

ID AAAT95155 standard; DNA; 17 BP.

AAAT95155;

18-FEB-1998 (first entry)

Human or monkey Ig heavy chain variable region primer VH1.



XX Old World monkey; immunoglobulin; Ig; heavy chain; CD4;  
 KW human; variable region; chimeric antibody;  
 KW B cell lymphoma; infectious disease; AIDS; autoimmune disease;  
 KW inflammatory disease; transplant rejection; imaging reagent;  
 KW vaccine; immunogen; immunotherapy; anti-idiotypic response;  
 KW immunosuppression; treatment; prevention; proliferative disease;  
 KW hyperproliferative disease; immunologically mediated disease;  
 KW rheumatoid arthritis; lupus erythematosus; PCR primer;  
 KW systemic lupus erythematosus; SLE; Hashimoto's thyroiditis;  
 KW multiple sclerosis; myasthenia gravis; type 1 diabetes; uveitis;  
 KW neoplastic syndrome; psoriasis; atopic dermatitis;  
 KW contact dermatitis; eczematous dermatitis; seborrheic dermatitis;  
 KW lichen planus; pemphigus; bullous pemphigus; Epidermolysis bullosa;  
 KW urticaria; angioedema; vasculitis; erythema;  
 KW cutaneous eosinophilia; alopecia areata;  
 KW reversible obstructive airways disease; intestinal inflammation;  
 KW intestinal allergy; Coeliac disease; proctitis; eosinophilia;  
 KW gastroenteritis; mastocytosis; Crohn's disease; ulcerative colitis;  
 KW food related allergy; migraine; rhinitis; eczema;  
 KW non-immunogenic; ss.  
 XX Synthetic;  
 OS Homo sapiens.  
 OS Cebus apella.  
 XX US5681722-A.  
 PN 28-OCT-1997.  
 PD 07-JUN-1995; 95US-0478039.  
 XX 10-JUL-1992; 92US-0912292.  
 XX 25-JUL-1991; 91US-0735064.  
 PR 23-MAR-1992; 92US-0856281.  
 PR 25-JAN-1995; 95US-0379072.  
 PR 07-JUN-1995; 95US-0478039.  
 XX (IDEC-) IDEC PHARM CORP.  
 PA Hanna N, Newman RA, Raab RW.  
 PI WPI: 1997-535052/49.  
 DR Production of humanised antibodies containing monkey variable region  
 PT - used for the treatment of B cell lymphoma, autoimmune disease,  
 PT inflammatory disease and infection, e.g. by HIV  
 XX Example 1; Fig 8; 84pp; English.  
 PS The present sequence is a PCR primer for a human or monkey  
 XX immunoglobulin heavy chain variable region cDNA, which  
 CC was used in the development of a novel method for producing a  
 CC chimeric antibody (Ab), comprising the variable region of an Old  
 CC World monkey (OWM) Ab and the constant region of a human Ab. The  
 CC method comprises amplifying DNA from the OWM using a primer  
 CC complementary to the 5' leader sequence of the OWM Ab gene and  
 CC fusing the resulting variable region coding sequence with a human  
 CC constant region coding sequence.  
 CC The chimeric Ab may be used as a passive or active therapeutic for  
 CC B cell lymphoma, infectious, e.g. AIDS, autoimmune and inflammatory  
 CC diseases and transplant rejection. The Ab can be used in its native  
 CC form or as part of an Ab/chelate, Ab/drug or Ab/toxin complex.  
 CC Additionally, a whole Ab, or a fragment (Fab2, Fab, Fv) may be used  
 CC as an imaging reagent or as a potential vaccine or immunogen in  
 CC active immunotherapy to generate anti-idiotypic responses.  
 CC An anti-CD4 recombinant Ab, or a fragment can also be used to  
 CC induce immunosuppression and can therefore be used to treat or  
 CC prevent resistance to, or rejection of transplanted organs or  
 CC tissues, autoimmune, inflammatory, proliferative and  
 CC hyperproliferative diseases, cutaneous manifestations of  
 CC immunologically mediated diseases (e.g. rheumatoid arthritis, lupus  
 CC erythematosus, systemic lupus erythematosus, Hashimoto's

CC thyroiditis, multiple sclerosis, myasthenia gravis, type 1  
 CC diabetes, uveitis, neoplastic syndrome, psoriasis, atopic  
 CC dermatitis, contact dermatitis and further eczematous dermatitis;  
 CC seborrheic dermatitis, lichen planus, pemphigus, bullous pemphigus,  
 CC epidermolysis bullosa, urticaria, angioedema, vasculitis,  
 CC erythema, cutaneous eosinophilias, alopecia areata), reversible  
 CC obstructive airways disease, intestinal inflammations and  
 CC allergies (e.g. Coeliac disease, proctitis, eosinophilia  
 CC gastroenteritis, mastocytosis, Crohn's disease and ulcerative  
 CC colitis) and food related allergies (e.g. migraine, rhinitis and  
 CC eczema).  
 CC The Ab of the invention is non-immunogenic and therefore does not  
 CC induce a human anti-Ab response. It also has a relatively long  
 CC half-life and a full effector function with human cells and  
 CC complement.  
 XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;  
 SQ Query Match 81.4%; Score 11.4; DB 18; Length 17;  
 Best Local Similarity 85.7%; Pred. No. 4.6e+03;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CAAGTCCAGNCCA 14  
 Db 17 CCAGTCCAGTCCA 4  
 RESULT 10  
 AAT91566/c  
 ID AAT91566 standard; DNA: 17 BP.  
 XX AAT91566;  
 AC 16-JAN-1998 (first entry)  
 XX Cynomolgus monkey heavy chain variable region primer VH1.  
 DE Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig;  
 KW chimpanzee; chimeric antibody; human therapy; Old World monkey;  
 KW antigen binding region; tumour; PCR; polymerase chain reaction; ss.  
 XX Synthetic.  
 OS US5658570-A.  
 PN 19-AUG-1997.  
 PD 25-JUL-1991; 91US-0735064.  
 PR 10-JUL-1992; 92US-0912292.  
 PR 25-JUL-1991; 91US-0735064.  
 PR 23-MAR-1992; 92US-0856281.  
 PR 25-JAN-1995; 95US-0379072.  
 XX (IDEC-) IDEC PHARM CORP.  
 PA Hanna N, Newman RA, Raab RW.  
 PI WPI: 1997-424183/39.  
 DR Chimeric antibodies for human therapy - comprising human or  
 PT chimpanzee immunoglobulin constant region and an Old World monkey  
 PT antigen-binding region  
 XX Example 1; Fig 8; 46pp; English.  
 PS A new chimeric antibody (Ab) has been developed comprising a human or  
 CC chimpanzee immunoglobulin (Ig) constant region and an Old World monkey  
 CC antigen (Ag)-binding region. An anti-CD4 antibody (Ab) comprising the  
 CC light- and heavy-chain variable regions encoded by AAT91564 and AAT91565  
 CC is also new. The present sequence represents a primer, VH1, used in the  
 CC amplification of cynomolgus monkey immunoglobulin heavy chain regions.  
 CC The Abs are useful for human therapy, especially of tumours. Old world

CC monkeys are sufficiently different from humans to allow Abs against  
CC human Abs, even relatively conserved Abs such as CD4 and CD54, to be  
CC raised in these monkeys, and are sufficiently similar to humans to avoid  
CC host anti-Ab immune responses when the Abs are introduced into humans.  
XX

SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;

Query Match 81.4%; Score 11.4; DB 18; Length 17;  
Best Local Similarity 85.7%; Pred. No. 4.6e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCAGNCCA 14  
1 | | | | | | | | | | | | | | | | | |  
Db 17 CCAGGTCAGTCACA 4

## RESULT 11

AA62902/C  
ID AAT62902 standard; DNA: 17 BP.

XX AAT62902;

DT 18-OCT-1997 (first entry)

DE VH1 heavy chain variable region.

XX CD4: monoclonal antibody; chimeric antibody; recombinant antibody;  
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;  
KW leukaemia; lymphoma; graft-versus-host disease; asthma;  
KW transplant rejection; HIV; therapy; CE9.1; ss.

XX Synthetic.

XX W09709351-A1.

XX 13-MAR-1997.

XX 05-SEP-1996; 96WO-US14324.

XX 06-SEP-1995; 95US-0523894.

PA (IDEC-) IDEC PHARM CORP.

PI Hanna N, Newman RA, Refl ME;

DR WPI: 1997-201913/18.

XX Chimeric antibody comprising monkey variable domains and human  
PT constant domains - affects CD4-mediated immune functions, esp.  
PT useful for treatment of autoimmune disease, e.g. rheumatoid  
PT arthritis

PS Disclosure; Fig 8; 15pp; English.

XX Sequences are provided for heavy chain variable regions VH1-VH6  
CC (AAT62902-07), heavy chain constant region Igm and IgG1-4 antisense  
CC strands (AAT62908-09), kappa and lambda light chain variable regions  
CC (AAT62910-11) and kappa and lambda light chain constant region  
CC antisense strands (AAT62912-13). Novel monoclonal and chimeric  
CC antibodies (see also AAW14924) comprise heavy and light chain  
CC variable regions (AAW14922-23) from macaque anti-human CD4 monoclonal  
CC antibody E9.1 and human gamma-1 or gamma-4 (AAW14925-27) constant  
CC regions.  
XX

SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;

Query Match 81.4%; Score 11.4; DB 18; Length 17;  
Best Local Similarity 85.7%; Pred. No. 4.6e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCAGNCCA 14  
1 | | | | | | | | | | | | | | | | | |  
Db 17 CCAGGTCAGTCACA 4

## RESULT 12

AAV31430/C  
ID AAV31430 standard; DNA: 17 BP.

XX AAV31430;

DT 10-AUG-1998 (first entry)

DE Cynomolgus immunoglobulin VH region amplifying primer VH1.

XX Anti-CD4 antibody; antigen-binding; treatment; chimeric; human;  
KW monkey; rheumatoid arthritis; psoriatic arthritis; PCR primer; ss.

XX Synthetic.

OS Macaca cynomolgus.

XX US5756096-A.

PD 26-MAY-1998.

XX 07-JUN-1995; 95US-0476237.

XX 07-JUN-1995; 95US-0476237.

XX 25-JUL-1991; 91US-0735064.

XX 23-MAR-1992; 92US-0856281.

XX 10-JUL-1992; 92US-0912282.

XX 25-JAN-1995; 95US-0379072.

XX (IDEC-) IDEC PHARM CORP.

PI Hanna N, Newman RA, Raab RW;

DR WPI: 1998-321461/28.

XX Treatment of rheumatoid and psoriatic arthritis - comprises  
PT administration of chimeric human-monkey anti-CD4 antibody  
PT Example 1; Fig 8; 47pp; English.

XX This primer is used for the PCR amplification of the heavy chain variable  
CC (VH) region of cynomolgus immunoglobulin sequence. This is used in the  
CC construction of a chimeric human-monkey anti-CD4 antibody. The antibody  
CC comprises antigen-binding sequences from an old world monkey antibody and  
CC human constant domain sequences. The antibody specifically binds to CD4  
CC and can be used in the treatment of rheumatoid or psoriatic arthritis.

SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;

Query Match 81.4%; Score 11.4; DB 19; Length 17;  
Best Local Similarity 85.7%; Pred. No. 4.6e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCAGNCCA 14  
1 | | | | | | | | | | | | | | | | | |  
Db 17 CCAGGTCAGTCACA 4

## RESULT 13

AAV23793/C  
ID AAV23793 standard; cDNA: 17 BP.

XX AAV23793;

DT 29-JUL-1998 (first entry)

DE Primer for Anti-CD4 antibody coding sequence fragment.

XX Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;  
KW Old World monkey; constant domain; eczema; immuno-modulated disease;  
KW rheumatoid arthritis; PCR primer; ss.

XX

OS Synthetic.  
OS Primate sp.  
PN US5750105-A.  
XX 12-MAY-1998.  
PD 07-JUN-1995; 95US-0476349.  
XX 10-JUL-1992; 92US-0912292.  
PR 25-JUL-1991; 91US-0735064.  
PR 23-MAR-1992; 92US-0856281.  
PR 05-DEC-1995; 95US-0379072.  
PR 07-JUN-1995; 95US-0476349.  
XX (IDEC-) IDEC PHARM CORP.  
PI Hanna N, Newman RA, Raab RW;  
DR WPI: 1998-296690/26.  
XX Improved method for antibody treatment - uses an antibody comprising  
PT an Old world monkey variable region and a human constant domain  
XX Example 1; Fig 8; 84pp; English.  
XX This sequence is a PCR primer for DNA encoding an anti-CD4 antibody  
CC (Ab). The amplified sequence can be used in the method of the invention  
CC for treating a subject, where the treatment comprises administration of  
CC an Ab. The method comprises the administration of an antibody which has  
CC to an antigen (Ag) (or Ag binding portion), and a human constant domain.  
CC The method is useful for the treatment of eczema and immuno-modulated  
CC diseases and especially rheumatoid arthritis. The recombinant antibodies  
CC used are sufficiently different from native monkey antibodies to allow  
CC human antigens to raise these antibodies, but similar enough to human  
CC antibody so there is no immune response to the antibodies in humans.  
CC Compared to antibodies used in therapy in prior art, these antibodies do  
CC not induce human anti-antibodies on repeated administration. They also  
CC have longer half-lives and do not have a lack of effector function with  
CC human cells.  
SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;  
Query Match 81.4%; Score 11.4; DB 19; Length 17;  
Best Local Similarity 85.7%; Pred. No. 4.6e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CAAGGTCAGNCCA 14  
DB 17 CCAGGTCAGTCCA 4  
RESULT 14  
AAV05683/C standard; DNA; 17 BP.  
XX AAV05683;  
AC 05-MAY-1998 (first entry)  
DT Human/monkey heavy chain variable region primer VHL.  
XX  
DE  
XX  
KW Primer: PCR: amplification; leader sequence; human; monkey; baboon;  
KW macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid;  
KW lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;  
KW tumour; antibody; ss.  
XX  
XX Synthetic;  
OS Homo sapiens.  
OS Macaca sp.  
OS Papio sp.  
XX

PN US5693780-A.  
XX 02-DEC-1997.  
PD 07-JUN-1995; 95US-0481869.  
XX 10-JUL-1992; 92US-0912292.  
PR 25-JUL-1991; 91US-0735064.  
PR 23-MAR-1992; 92US-0856281.  
PR 25-JAN-1995; 95US-0379072.  
PR 07-JUN-1995; 95US-0481869.  
XX (IDEC-) IDEC PHARM CORP.  
PI Hanna N, Newman RA, Raab RW;  
DR WPI: 1998-031820/03.  
XX Nucleic acid encoding hybrid antibody - comprising monkey  
PT antigen-binding region and human or chimp constant region  
XX Example 1; Fig 8; 46pp; English.  
XX This sequence represents a sense primer derived by comparing sequences  
CC from human and monkey (especially baboon (Papio sp.) and macaque  
CC (Macaca sp.)) immunoglobulin (Ig) heavy chain regions. The primer is  
CC used to amplify the monkey heavy chain variable region for construction  
CC of a recombinant antibody comprising: (i) an Old World monkey Ig  
CC antigen-binding region; and (ii) a human or chimpanzee Ig constant  
CC region. The hybrid antibodies can be used as passive or active  
CC therapeutic agents against human diseases, e.g. B-cell lymphoma, AIDS,  
CC autoimmune and inflammatory diseases, transplant rejection or tumours,  
CC or for producing therapeutic and diagnostic conjugates. Although  
CC evolutionary distant monkeys are used to raise antibodies against human  
CC antigens, they are sufficiently similar that they produce antibodies  
CC similar to human antibodies, such when the monkey antibodies are  
CC introduced into humans, no host anti-antibody response is stimulated.  
SQ Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;  
Query Match 81.4%; Score 11.4; DB 19; Length 17;  
Best Local Similarity 85.7%; Pred. No. 4.6e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CAAGGTCAGNCCA 14  
DB 17 CCAGGTCAGTCCA 4  
RESULT 15  
AAT43427/C standard; DNA; 18 BP.  
XX AAT43427;  
AC 17-FEB-1997 (first entry)  
DT VHL family specific primer for human heavy chain Ig.  
XX  
DE  
XX  
KW xenograft rejection; xenotransplantation; organ transplant;  
KW animal model; pig; monoclonal antibody; primer; PCR;  
KW polymerase chain reaction; phage display; ss.  
XX  
XX Synthetic.  
OS WO9636358-A1.  
PN 21-NOV-1996.  
PD 14-MAY-1996; 96WO-US06804.  
PF 15-MAY-1995; 95US-0440621.  
PR  
XX

PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
 XX  
 PI Cramer DV, Makowka L, Wu G;  
 XX  
 DR WPI: 1997-011852/01.  
 XX

PT Inhibiting xenograft rejection by modifying antigen expression of  
 PT the graft - prevents binding of anti-donor antibody and prolongs  
 PT graft survival  
 XX

PS Example 16; Page 121; 135pp; English.  
 XX

CC PCR primers VH1-VH6 (AAT43427-32) are Ig family specific heavy chain  
 CC 5' primers designed for the amplification of antibody VH region  
 CC cDNA and for the introduction of cohesive termini compatible with  
 CC directional ligation into the unique NotI or SpeI sites of the  
 CC SurZAP vector. They were used with 3' primers in the PCR  
 CC amplification of antibody heavy chain variable region cDNA from  
 CC lymphocytes of a human transplant patient who had received a  
 CC porcine xenograft. A human IgM heavy chain, human Igk light  
 CC chain Fab library was generated using phage display and panned for  
 CC anti-donor xenograft antibody sequences.  
 XX

SQ Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 other;

Query Match 81.4%; Score 11.4; DB 18; Length 18;  
 Best Local Similarity 85.7%; Pred. No. 4.6e+03;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCCAGNCCA 14  
 I | | | | | | | | | |  
 DB 17 CCAGGTCCAGTCCA 4

Search completed: June 21, 2003, 22:26:29  
 Job time : 78.7812 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 ; Search time 16.625 Seconds  
(without alignments)  
258.254 Million cell updates/sec

Title: US-09-964-666-14  
Perfect score: 14  
Sequence: 1 CAAGCTCCAGNCCA 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/lna/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/lna/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/PTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
C 1	11.4	81.4	17	1	US-08-379-072A-5 Sequence 5, Appl
C 2	11.4	81.4	17	1	US-08-478-039-51 Sequence 51, Appl
C 3	11.4	81.4	17	1	US-08-481-869-5 Sequence 5, Appl
C 4	11.4	81.4	17	1	US-08-476-349A-51 Sequence 51, Appl
C 5	11.4	81.4	17	1	US-08-476-237-1 Sequence 1, Appl
C 6	11.4	81.4	17	3	US-08-523-894-44 Sequence 44, Appl
C 7	11.4	81.4	22	4	US-09-320-095-13 Sequence 13, Appl
C 8	11.4	81.4	22	4	US-09-523-487-13 Sequence 13, Appl
C 9	11.4	81.4	26	1	US-08-478-039-20 Sequence 20, Appl
C 10	11.4	81.4	26	1	US-08-476-349A-20 Sequence 20, Appl
C 11	11.4	81.4	26	3	US-08-523-894-13 Sequence 13, Appl
C 12	11.4	81.4	27	2	US-08-646-367-3 Sequence 3, Appl
C 13	11.4	81.4	30	2	US-08-373-190-59 Sequence 59, Appl
C 14	11.4	81.4	30	2	US-08-438-190A-59 Sequence 59, Appl
C 15	11.4	81.4	30	3	US-08-803-085-14 Sequence 14, Appl
C 16	11.4	81.4	30	3	US-09-287-145A-59 Sequence 59, Appl
C 17	11.4	81.4	30	4	US-09-556-111-59 Sequence 59, Appl
C 18	11.4	81.4	34	3	US-08-814-412-21 Sequence 21, Appl
C 19	11.4	81.4	35	5	PCT-US94-14106-23 Sequence 23, Appl
C 20	11.4	81.4	38	1	US-08-026-320A-5 Sequence 5, Appl
C 21	11.4	81.4	38	2	US-08-761-277A-52 Sequence 52, Appl
C 22	11.4	81.4	46	2	US-07-916-098A-60 Sequence 60, Appl
C 23	10.4	74.3	15	4	US-09-081-646-339 Sequence 339, App
C 24	10.4	74.3	20	3	US-09-184-658-24 Sequence 24, Appl
C 25	10.4	74.3	20	3	US-09-184-658-25 Sequence 25, Appl
C 26	10.4	74.3	20	3	US-09-289-267-64 Sequence 64, Appl
C 27	10.4	74.3	21	2	US-08-437-607A-28 Sequence 28, Appl

C 28	10.4	74.3	21	4	US-08-949-155-16 Sequence 16, Appl
C 29	10.4	74.3	21	4	US-09-819-964-16 Sequence 16, Appl
C 30	10.4	74.3	22	4	US-09-487-792-50 Sequence 50, Appl
C 31	10.4	74.3	24	2	US-08-691-814B-53 Sequence 53, Appl
C 32	10.4	74.3	25	4	US-09-462-136-10 Sequence 10, Appl
C 33	10.4	74.3	26	2	US-08-859-998-653 Sequence 653, App
C 34	10.4	74.3	26	4	US-09-225-928-653 Sequence 653, App
C 35	10.4	74.3	28	5	PCT-US94-10957-19 Sequence 19, Appl
C 36	10.4	74.3	30	2	US-08-924-440-4 Sequence 4, Appl
C 37	10.4	74.3	39	6	5187077-19 Patent No. 5187077
C 38	10.4	74.3	39	6	5427925-17 Patent No. 5427925
C 39	10.4	74.3	43	3	US-08-589-939-61 Sequence 61, Appl
C 40	10	71.4	20	1	US-07-767-135-17 Sequence 17, Appl
C 41	10	71.4	20	1	US-07-841-652-8 Sequence 8, Appl
C 42	10	71.4	20	3	US-09-289-267-65 Sequence 65, Appl
C 43	10	71.4	20	4	US-09-746-694-40 Sequence 40, Appl
C 44	10	71.4	22	1	US-08-379-081B-314 Sequence 314, App
C 45	10	71.4	22	1	US-08-379-078-314 Sequence 314, App

## ALIGNMENTS

RESULT 1  
US-08-379-072A-5/c  
; Sequence 5, Application US/08379072A  
; Patent No. 5658570  
; GENERAL INFORMATION:  
; APPLICANT: NEWMAN, Roland A.  
; APPLICANT: HANNA, Nabil  
; APPLICANT: RAMB, Ronald W.  
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/379, 072A  
; FILING DATE: 25-JAN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/912,292  
; FILING DATE: 10-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/856,281  
; FILING DATE: 23-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,064  
; FILING DATE: 23-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rea, Teresa Stanek  
; REGISTRATION NUMBER: 30,427  
; REFERENCE/DOCKET NUMBER: 012712-067  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-379-072A-5

Query Match 81.4%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 85.7%; Pred. No. 5.8e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGTCAGNCCA 14  
17 CCAGGTCAGTCCA 4

## RESULT 2

US-08-478-039-51/c  
; Sequence 51, Application US/08478039  
; Patent No. 5681722  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Hanna, Nabil W.  
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,039  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/379,072  
; FILING DATE: 25-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/912,292  
; FILING DATE: 10-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/856,281  
; FILING DATE: 23-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,064  
; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin Esq., Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-160  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; ANTI-SENSE: NO  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: heavy chain variable region  
; US-08-478-039-51

Query Match 81.4%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 85.7%; Pred. No. 5.8e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGTCAGNCCA 14  
17 CCAGGTCAGTCCA 4

Db 17 CCAGGTCAGTCCA 4

## RESULT 3

US-08-481-869-5/c  
; Sequence 5, Application US/08481869  
; Patent No. 5693780  
; GENERAL INFORMATION:  
; APPLICANT: NEWMAN, Roland A.  
; APPLICANT: HANNA, Nabil W.  
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481,869  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/379,072A  
; FILING DATE: 25-JAN-1995  
; APPLICATION NUMBER: US/07/912,292  
; FILING DATE: 10-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/856,281  
; FILING DATE: 23-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,064  
; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rea, Teresa Stanek  
; REGISTRATION NUMBER: 30,427  
; REFERENCE/DOCKET NUMBER: 012712-067  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-481-869-5

Query Match 81.4%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 85.7%; Pred. No. 5.8e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGTCAGNCCA 14  
17 CCAGGTCAGTCCA 4

## RESULT 4

US-08-476-349A-51/c  
; Sequence 51, Application US/08476349A  
; Patent No. 5750105  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Hanna, Nabil W.  
; APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince St.  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,349A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/379,072  
FILING DATE: 25-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/912,292  
FILING DATE: 10-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,281  
FILING DATE: 23-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/735,064  
FILING DATE: 25-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin Esq., Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-161  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
ANTI-SENSE: NO  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: heavy chain variable region  
US-08-476-349A-51  
Query Match 81.4%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 85.7%; Pred. No. 5.8e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CAAGTCCAGNCCA 14  
Db 17 CCAGTCCAGTCCA 4  
RESULT 5  
US-08-476-237-1/C  
Sequence 1, Application US/08476237  
Patent No. 5756096  
GENERAL INFORMATION:  
APPLICANT: NEWMAN, Roland A.  
APPLICANT: HANNA, Nabil  
APPLICANT: RAAB, Ronald W.  
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia

COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,237  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,281  
FILING DATE: 23-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/735,064  
FILING DATE: 25-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-6620  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-476-237-1  
Query Match 81.4%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 85.7%; Pred. No. 5.8e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CAAGTCCAGNCCA 14  
Db 17 CCAGTCCAGTCCA 4  
RESULT 6  
US-08-523-894-44/C  
Sequence 44, Application US/08523894  
Patent No. 6136310  
GENERAL INFORMATION:  
APPLICANT: Hanna, Nabil  
APPLICANT: Newman, Roland A.  
APPLICANT: Reff, Mitchell E.  
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/523,894  
FILING DATE: 06-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VHL heavy chain variable region
; US-08-523-894-44

Query Match      81.4%; Score 11.4; DB 3; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.8e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CAAGGTCAGNCCA 14
Db      17 CCAGGTCAGTCCA 4

RESULT 7
US-09-320-095-13
; Sequence 13, Application US/09320095
; Patent No. 6087473
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS
; FILE REFERENCE: 98-22
; CURRENT APPLICATION NUMBER: US/09/320,095
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: US 60/087,032
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer ZC15,999
; US-09-320-095-13

Query Match      81.4%; Score 11.4; DB 3; Length 22;
Best Local Similarity 85.7%; Pred. No. 5.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CAAGGTCAGNCCA 14
Db      5 CAAGGTCAGAGCA 18

RESULT 8
US-09-523-487-13
; Sequence 13, Application US/09523487
; Patent No. 6232098
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS
; FILE REFERENCE: 98-22
; CURRENT APPLICATION NUMBER: US/09/523,487
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/320,095
; PRIOR FILING DATE: 1999-05-26

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```

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer ZC15,999
; US-09-523-487-13

Query Match      81.4%; Score 11.4; DB 4; Length 22;
Best Local Similarity 85.7%; Pred. No. 5.9e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CAAGGTCAGNCCA 14
Db      5 CAAGGTCAGAGCA 18

RESULT 9
US-08-478-039-20/c
; Sequence 20, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

```



ORGANISM: Homo sapiens or Monkey  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: heavy chain primers with SalI site  
US-08-478-039-20

Query Match 81.4%; Score 11.4; DB 1; Length 26;  
Best Local Similarity 85.7%; Pred. No. 6e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
| | | | | | | | | | | | | | | | | |  
Db 26 CCAGTCCAGTCCA 13

RESULT 10  
US-08-476-349A-20/C  
Sequence 20, Application US/08476349A  
Patent No. 5750105  
GENERAL INFORMATION:  
APPLICANT: Newman, Roland A.  
APPLICANT: Hanna, Nabli  
APPLICANT: Raab, Ronald W.  
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince St.  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,349A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/379,072  
FILING DATE: 25-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/912,292  
FILING DATE: 10-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,281  
FILING DATE: 23-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/735,064  
FILING DATE: 25-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin Esq., Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-161  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens or Monkey  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: heavy chain primers with SalI site  
US-08-476-349A-20

Query Match 81.4%; Score 11.4; DB 1; Length 26;  
Best Local Similarity 85.7%; Pred. No. 6e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
| | | | | | | | | | | | | | | | | |  
Db 26 CCAGTCCAGTCCA 13

RESULT 11  
US-08-523-894-13/C  
Sequence 13, Application US/08523894  
Patent No. 6136310  
GENERAL INFORMATION:  
APPLICANT: Hanna, Nabli  
APPLICANT: Newman, Roland A.  
APPLICANT: Reif, Mitchell E.  
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
TITLE OF INVENTION: Therapy  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/523,894  
FILING DATE: 06-SEP-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human or Monkey  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: VH1 leader sequence  
US-08-523-894-13

Query Match 81.4%; Score 11.4; DB 3; Length 26;  
Best Local Similarity 85.7%; Pred. No. 6e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
| | | | | | | | | | | | | | | | | |  
Db 26 CCAGTCCAGTCCA 13

RESULT 12  
US-08-646-367-3/C  
Sequence 3, Application US/08646367  
Patent No. 5959085  
GENERAL INFORMATION:  
APPLICANT: Pierre Garrone  
APPLICANT: Odile Djossou

APPLICANT: Francois Fossiez  
APPLICANT: Jacques Bancheureau  
TITLE OF INVENTION: Human Monoclonal Antibodies  
TITLE OF INVENTION: Against Human Cytokines And  
TITLE OF INVENTION: Methods Of Making And Using Such Antibodies  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESS: Schering-Plough Corporation  
STREET: 2000 Gallopings Hill Road  
CITY: Kenilworth  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07033  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.5.3  
SOFTWARE: Microsoft Word 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,367  
FILING DATE: May 16, 1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Foulke, Cynthia L.  
REGISTRATION NUMBER: 32,364  
REFERENCE/DOCKET NUMBER: SF0403K  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-298-2987  
TELEFAX: 908-298-5388  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-646-367-3

Query Match 81.4%; Score 11.4; DB 2; Length 27;  
Best Local Similarity 85.7%; Pred. No. 6e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
DB 24 CCAGTCCAGTCCA 11

RESULT 13  
US-08-373-190-59/C  
Sequence 59, Application US/08373190  
Patent No. 5851829  
GENERAL INFORMATION:  
APPLICANT: MARASCO, WAYNE  
APPLICANT: HASSETT, WILLIAM  
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/373,190  
FILING DATE: 17-JAN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06735

FILING DATE: 16-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: RESNICK, DAVID S  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 41956-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: STRE UR 2002  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-373-190-59

Query Match 81.4%; Score 11.4; DB 2; Length 30;  
Best Local Similarity 85.7%; Pred. No. 6.1e+02;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
DB 27 CCAGTCCAGTCCA 14

RESULT 14  
US-08-438-190A-59/C  
Sequence 59, Application US/08438190A  
Patent No. 5963371  
GENERAL INFORMATION:  
APPLICANT: MARASCO, WAYNE  
APPLICANT: HASSETT, WILLIAM  
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &  
ADDRESSEE: CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,190A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: EISENSTEIN, RONALD T.  
REGISTRATION NUMBER: 30628  
REFERENCE/DOCKET NUMBER: 41956  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-438-190A-59

Query Match 81.4%; Score 11.4; DB 2; Length 30;  
 Best Local Similarity 85.7%; Pred. No. 6.1e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
 | | | | | | | | | | | | | | | |  
 Db 27 CCAGTCCAGTCCA 14

RESULT 15

US-08-803-085-14/c  
 ; Sequence 14, Application US/08803085  
 ; Patent No. 6011138

GENERAL INFORMATION:

APPLICANT: KLOETZER, William S.  
 APPLICANT: MAKIURA, Takehiko  
 TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL  
 TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 STREET: P.O. Box 1404  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/803,085  
 FILING DATE: 20-FEB-1997  
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.  
 REGISTRATION NUMBER: 35,030  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 836-6620  
 TELEFAX: (703) 836-2021

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 14:  
 LENGTH: 30 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-803-085-14

Query Match 81.4%; Score 11.4; DB 3; Length 30;  
 Best Local Similarity 85.7%; Pred. No. 6.1e+02;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
 | | | | | | | | | | | | | | | |  
 Db 30 CCAGTCCAGTCCA 17

Search completed: June 22, 2003, 00:01:38  
 Job time: 18.625 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 22:26:37 ; Search time 41.3438 seconds  
(without alignments)  
496.907 Million cell updates/sec

Title: US-09-964-666-14

Perfect score: 14  
Sequence: 1 CAAGGTCAGNCCA 14

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Published\_Applications\_NA.\*  
2: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	13	92.9	14	US-09-964-667-14	Sequence 14, Appl
2	13	92.9	14	US-09-964-666-14	Sequence 14, Appl
3	13	92.9	14	US-09-964-412-14	Sequence 14, Appl
4	12	85.7	24	US-09-940-185-281	Sequence 281, Appl
5	12	85.7	25	US-09-940-185-4261	Sequence 4261, Appl
6	11.4	81.4	17	US-10-211-357-44	Sequence 44, Appl
7	11.4	81.4	17	US-09-850-165-1	Sequence 1, Appl
8	11.4	81.4	18	US-10-067-790-16	Sequence 16, Appl
9	11.4	81.4	18	US-10-067-892-16	Sequence 16, Appl
10	11.4	81.4	18	US-09-539-382-16	Sequence 16, Appl
11	11.4	81.4	18	US-10-067-893-16	Sequence 16, Appl
12	11.4	81.4	20	US-10-024-018-2	Sequence 2, Appl
13	11.4	81.4	22	US-09-927-121B-38	Sequence 38, Appl
14	11.4	81.4	25	US-10-215-112-10872	Sequence 10872, A
15	11.4	81.4	26	US-10-211-357-13	Sequence 13, Appl
16	11.4	81.4	26	US-09-850-165-42	Sequence 42, Appl
17	11.4	81.4	30	US-10-103-686-14	Sequence 14, Appl
18	11.4	81.4	30	US-09-019-441-14	Sequence 14, Appl
19	11.4	81.4	35	US-09-825-805-218	Sequence 218, Appl

20	11.4	81.4	37	US-09-825-805-219	Sequence 219, Appl
21	11.4	81.4	38	US-09-925-664-52	Sequence 52, Appl
22	11.4	81.4	38	US-09-825-805-954	Sequence 954, Appl
23	11.4	81.4	38	US-09-825-805-987	Sequence 987, Appl
24	11.4	81.4	38	US-09-825-805-1106	Sequence 1106, Appl
25	11.4	81.4	38	US-09-930-423-2985	Sequence 2985, Appl
26	11.4	81.4	39	US-09-971-980-21	Sequence 21, Appl
27	11.4	81.4	39	US-10-098-263B-45863	Sequence 45863, A
28	10.6	75.7	31	US-09-801-274-1163	Sequence 1163, Appl
29	10.4	74.3	17	US-09-864-636A-2609	Sequence 2609, Appl
30	10.4	74.3	20	US-10-087-323-19	Sequence 19, Appl
31	10.4	74.3	20	US-09-906-032A-3	Sequence 3, Appl
32	10.4	74.3	25	US-10-215-112-6573	Sequence 6573, Appl
33	10.4	74.3	25	US-10-208-731-10	Sequence 10, Appl
34	10.4	74.3	25	US-09-864-636A-2607	Sequence 2607, Appl
35	10.4	74.3	25	US-10-098-263B-35397	Sequence 35397, A
36	10.4	74.3	25	US-10-098-263B-35398	Sequence 35398, A
37	10.4	74.3	25	US-10-098-263B-35907	Sequence 35907, A
38	10.4	74.3	25	US-10-098-263B-51690	Sequence 51690, A
39	10.4	74.3	25	US-10-098-263B-57464	Sequence 57464, A
40	10.4	74.3	25	US-10-098-263B-59924	Sequence 59924, A
41	10.4	74.3	25	US-10-098-263B-62519	Sequence 62519, A
42	10.4	74.3	25	US-10-098-263B-62978	Sequence 62978, A
43	10.4	74.3	25	US-10-098-263B-81538	Sequence 81538, A
44	10.4	74.3	25	US-10-098-263B-89716	Sequence 89716, A
45	10.4	74.3	25	US-10-098-263B-102710	Sequence 102710, A

# ALIGNMENTS

RESULT 1  
US-09-964-667-14  
Sequence 14, Application US/09964667  
Publication No. US20030033621A1  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
Mands, Jack R.  
TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/964,667  
FILING DATE: 28-Sep-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0609,4370000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-964-667-14

Query Match 92.9%; Score 13; DB 9; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGTCCAGNCCA 14

DB 1 CAAGGTCCAGNCCA 14

RESULT 2

US-09-964-666-14

Sequence 14, Application US/09964666

Patent No. US20020104108A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/964,666

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-964-666-14

Query Match 92.9%; Score 13; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14

DB 1 CAAGTCCAGNCCA 14

RESULT 3

US-09-964-412-14

Sequence 14, Application US/09964412

Patent No. US20020129391A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/964,412

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-964-412-14

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/964,412

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-964-412-14

Query Match 92.9%; Score 13; DB 10; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14

DB 1 CAAGTCCAGNCCA 14

RESULT 4

US-09-940-185-281/C

Sequence 281, Application US/09940185

Publication No. US20030096239A1

GENERAL INFORMATION:

APPLICANT: Gunderson, Kevin

Chee, Mark

TITLE OF INVENTION: Probes and Decoder Oligonucleotides

FILE REFERENCE: A-69605-1

CURRENT APPLICATION NUMBER: US/09/940,185

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: US 60/227,948

PRIOR FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/228,854

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 4768

SOFTWARE: Patentin version 3.1

SEQ ID NO 281

LENGTH: 24

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Computer Generated Probe Sequence.

US-09-940-185-281

Query Match 85.7%; Score 12; DB 9; Length 24;

Best Local Similarity 92.3%; Pred. No. 1.8e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCC 13  
19 CAAGTCCAGACC 7

RESULT 5  
US-09-940-185-4261/c  
; Sequence 4261, Application US/09940185  
; Publication No. US20030096239A1  
; GENERAL INFORMATION:  
; APPLICANT: Gunderson, Kevin  
; APPLICANT: Chee, Mark  
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides  
; FILE REFERENCE: A-69605-1  
; CURRENT APPLICATION NUMBER: US/09/940,185  
; CURRENT FILING DATE: 2001-08-27  
; PRIOR APPLICATION NUMBER: US 60/227,948  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/228,854  
; PRIOR FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 4768  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 4261  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Computer Generated Probe Sequence.  
US-09-940-185-4261

Query Match 85.7%; Score 12; DB 9; Length 25;  
Best Local Similarity 92.3%; Pred. No. 1.8e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCC 13  
20 CAAGTCCAGACC 8

RESULT 6  
US-10-211-357-44/c  
; Sequence 44, Application US/10211357  
; Publication No. US20030077275A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanna, Nabil  
; Ref. Mitchell E.  
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
; Therapy  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314-3187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/211,357  
; FILING DATE: 05-Aug-2002  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/612,914A  
; FILING DATE: 10-Jul-2000  
; APPLICATION NUMBER: US 08/523,894  
; FILING DATE: 06-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: NO  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: VH1 heavy chain variable region  
SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
US-10-211-357-44

Query Match 81.4%; Score 11.4; DB 9; Length 17;  
Best Local Similarity 85.7%; Pred. No. 4e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
17 CCAGTCCAGTCCA 4

RESULT 7  
US-09-850-165-1/c  
; Sequence 1, Application US/09850165  
; Patent No. US20020150580A1  
; GENERAL INFORMATION:  
; APPLICANT: NEWMAN, ROLAND A.  
; APPLICANT: HANNA, NABIL  
; APPLICANT: RAAB, RONALD W.  
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY  
; FILE REFERENCE: 037003-0280614  
; CURRENT APPLICATION NUMBER: US/09/850,165  
; CURRENT FILING DATE: 2001-05-08  
; PRIOR APPLICATION NUMBER: 09/082,472  
; PRIOR FILING DATE: 1998-05-21  
; PRIOR APPLICATION NUMBER: 08/476,237  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/397,072  
; PRIOR FILING DATE: 1995-04-17  
; PRIOR APPLICATION NUMBER: 07/912,292  
; PRIOR FILING DATE: 1992-07-10  
; PRIOR APPLICATION NUMBER: 07/856,281  
; PRIOR FILING DATE: 1992-03-23  
; PRIOR APPLICATION NUMBER: 07/735,064  
; PRIOR FILING DATE: 1991-07-25  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 1  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-850-165-1

Query Match 81.4%; Score 11.4; DB 10; Length 17;  
Best Local Similarity 85.7%; Pred. No. 4e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14  
17 CCAGTCCAGTCCA 4

RESULT 8  
US-10-067-790-16/c  
; Sequence 16, Application US/10067790

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Publication No. US20030035807A1
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Allison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
APPLICANT: TURPEN, Thomas
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CAN
FILE REFERENCE: 18696-169194
CURRENT APPLICATION NUMBER: US/10/067,790
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/522,900
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 60/155,579
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: primer
US-10-067-790-16
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Query Match 81.4%; Score 11.4; DB 9; Length 18;

Best Local Similarity 85.7%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CAAGTCCAGNCCA 14
    | | | | | | | | | |
Db 15 CCAGTCCAGTCCA 2
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RESULT 9
US-10-067-892-16/c
Sequence 16, Application US/10067892
Publication No. US20030039659A1
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Allison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
APPLICANT: TURPEN, Thomas
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS
FILE REFERENCE: 18696-169194
CURRENT APPLICATION NUMBER: US/10/067,892
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/522,900
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: primer
US-10-067-892-16
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Query Match 81.4%; Score 11.4; DB 9; Length 18;

Best Local Similarity 85.7%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CAAGTCCAGNCCA 14
    | | | | | | | | | |
Db 15 CCAGTCCAGTCCA 2
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RESULT 10
US-09-539-382-16/c
Sequence 16, Application US/09539382
Publication No. US20030044417A1
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Allison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
APPLICANT: TURPEN, Thomas
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER
FILE REFERENCE: 18696-169195
CURRENT APPLICATION NUMBER: US/09/539,382
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 60/155,579
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: primer
US-09-539-382-16
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Query Match 81.4%; Score 11.4; DB 9; Length 18;

Best Local Similarity 85.7%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CAAGTCCAGNCCA 14
    | | | | | | | | | |
Db 15 CCAGTCCAGTCCA 2
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RESULT 11
US-10-067-893-16/c
Sequence 16, Application US/10067893
Publication No. US20030044420A1
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Allison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
APPLICANT: TURPEN, Thomas
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER
FILE REFERENCE: 18696-169194
CURRENT APPLICATION NUMBER: US/10/067,893
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/522,900
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 60/155,579
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: primer
US-10-067-893-16
```

Query Match 81.4%; Score 11.4; DB 9; Length 18;

Best Local Similarity 85.7%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CAAGTCCAGNCCA 14
```





CHROMOSOME/SEGMENT: VH1 leader sequence  
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-10-211-357-13

Query Match 81.4%; Score 11.4; DB 9; Length 26;  
 Best Local Similarity 85.7%; Pred. No. 3.8e+03;  
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCAGNCCA 14  
 | | | | | | | | | |  
 DB 26 CCAGGTCAGTCCA 13

Search completed: June 22, 2003, 03:18:25  
 Job time : 43.3438 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:28:37 ; Search time 604.734 Seconds  
(without alignments)  
374.936 Million cell updates/sec

Title: US-09-964-666-14

Sequence: 1 CAAGCTCCAGNCCA 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estbda:\*  
2: em\_esthum:\*  
3: em\_estnu:\*  
4: em\_estnu:\*  
5: em\_estrov:\*  
6: em\_estrpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hic:\*  
12: gb\_estl3:\*  
13: gb\_estl4:\*  
14: gb\_estl5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11.4	81.4	49	10	BE282036 601102010
2	11.4	81.4	50	10	AV428742 AV428742
3	11	78.6	50	14	H55190 H55190
4	10.4	74.3	19	17	A2825396 A2825396
5	10.4	74.3	31	17	A2437960 A2437960
6	10.4	74.3	46	13	B1908094 B1908094

Result No.	Score	Query Match	Length	ID	Description
7	10.4	74.3	50	9	AU107443
8	10	71.4	20	17	A2819886
9	10	71.4	34	9	AA669941
10	10	71.4	35	12	BF036425
11	10	71.4	42	14	T48919
12	10	71.4	44	17	A2489056
13	10	71.4	46	17	D86886
14	10	71.4	50	9	AU102541
15	10	71.4	50	9	AU102547
16	10	71.4	50	9	AU103657
17	10	71.4	50	9	AU103659
18	9.8	70.0	25	17	A2643950
19	9.8	70.0	28	17	A2327470
20	9.8	70.0	28	17	TA163A01P
21	9.8	70.0	29	17	A2492566
22	9.8	70.0	32	17	A2990287
23	9.8	70.0	38	17	TA130F07P
24	9.8	70.0	39	17	A2659162
25	9.8	70.0	40	9	AA880280
26	9.8	70.0	43	17	BH790549
27	9.8	70.0	47	13	BI221669
28	9.8	70.0	48	17	A2485794
29	9.8	70.0	49	9	AA876193
30	9.8	70.0	49	9	AA887238
31	9.8	70.0	49	9	A1457977
32	9.8	70.0	50	9	AU103167
33	9.8	70.0	50	9	AU106721
34	9.8	70.0	50	9	AU106942
35	9.8	70.0	50	14	N34794
36	9.4	67.1	22	17	A2389506
37	9.4	67.1	23	17	A2307822
38	9.4	67.1	23	17	A2480676
39	9.4	67.1	23	17	A2785457
40	9.4	67.1	32	17	A2456295
41	9.4	67.1	32	17	A2793160
42	9.4	67.1	33	17	A2791392
43	9.4	67.1	34	13	BJ034722
44	9.4	67.1	37	9	A1180523
45	9.4	67.1	37	9	A1815205

## ALIGNMENTS

RESULT 1  
BE282036/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BE282036 49 bp mRNA linear EST 26-OCT-2000  
601102010F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:349431 5',  
mRNA sequence.  
BE282036  
BE282036.1 GI:9157330  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclerogonathii; Muridae; Murinae; Mus.  
1 (bases 1 to 49)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LIAW543 row: C column: 04  
High quality sequence start: 2  
High quality sequence stop: 49.  
Location/Qualifiers

```

source
1. .49
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="3494331"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
stem cell origin."
/lab_host="DHI0B"
/notes="Organ: Lung; Vector: pCMV-Sport6; Site_1: Salt.
Site_2: NCI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT
2 a 27 g 9 t
ORIGIN
Query Match 81.4% Score 11.4; DB 10; Length 49;
Best Local Similarity 85.7% Pred. NO. 4.2e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CAAGTCCAGNCCA 14
||||| ||||| |||
DB 27 CAAGTCCAGGCCA 14

RESULT 2
LOCUS AVA28742 50 bp mRNA Linear EST 02-MAY-2000
DEFINITION japonicus young plants (two-week old) Lotus
cDNA clone MM0035d10_r 5', mRNA sequence.
AV28742
AV428742.1 GI:7678124
EST.
Lotus japonicus.
Lotus japonicus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.
1 (bases 1 to 50)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a
legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
20277479
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizuekazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
LOCATION/Qualifiers
1. .50
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MM0035d10_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/notes="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; Isolate=MIYakojima MG-20"
BASE COUNT
22 a 11 c 7 g 10 t
ORIGIN
Query Match 81.4% Score 11.4; DB 10; Length 50;
Best Local Similarity 85.7% Pred. NO. 4.2e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CAAGTCCAGNCCA 14
||||| ||||| |||
DB 17 CAAGTCCAGGCCA 30

RESULT 3
LOCUS H55190

```

LOCUS	H55190	50 bp	mRNA	Linear	EST 07-DEC-1995
DEFINITION	CH220129	Chromosome 22	exon	Homo sapiens	CDNA clone C22_166 5',
ACCESSION	H55190				
VERSION	H55190.1	GI:1108056			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 50) Trofatter,J.A., Long,K.R., Murrell,J.R., Stotler,C.J., Gusella,J.F., and Buckler,A.J.				
TITLE	An expression-independent catalog of genes from human chromosome 22				
JOURNAL	Genome Res. 5 (3), 214-224 (1995)				
MEDLINE	96159527				
COMMENT	Contact: Buckler AJ Molecular Neurogenetics Unit Massachusetts General Hospital Building 149, 13th St., Charlestown MA 02129 Tel: 6177249616 Fax: 6177265736 Email: buckler@helix.mgh.harvard.edu Seq primer: T3.				
FEATURES	Location/Qualifiers				
SOURCE	1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="C22_166" /clone_1ib="Chromosome 22 exon" /lab_host="E. coli DH5a" /note="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2: Bam HI (destroyed); Exons were isolated from human chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bgl II and subsequently cloned into pBluescriptIIKS+ at the Sal I and Bam HI sites."				
BASE COUNT	18 a 12 c 11 g . 9 t				
ORIGIN					
Query Match	78.6%; Score 11; DB 14; Length 50;				
Best Local Similarity	91.7%; Pred. No. 6.8e+04;				
Matches	11: Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	3 AGGTCACAGNCCA 14 				
Db	29 AGGTCACAGACA 40				
RESULT 4					
A2825396/c	A2825396	19 bp	DNA	linear	GSS 20-FEB-2001
LOCUS	2M0100N04R	Mouse 10kb	plasmid	UUC1M	library
DEFINITION	clone UUCG2M0100N04 R, DNA sequence.				
ACCESSION	A2825396				
VERSION	A2825396.1	GI:12995304			
KEYWORDS	GSS.				
SOURCE	mus musculus.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 19) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb				
JOURNAL	plasmid inserts				
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah				

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0100 row: N column: 04  
Seq primer: CACACAGAAACAGCATATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

source

1. 19  
Location/Qualifiers

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0100N04"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

2 a 9 c 3 g 5 t

## ORIGIN

Query Match 74.3%; Score 10.4; DB 17; Length 19;  
Best Local Similarity 84.6%; Pred. No. 1.1e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAGTCCAGNCCA 14  
|||||

DB 19 AAGTCCAGGCGCA 7

## RESULT 5

AZ437960/C

LOCUS AZ437960 31 bp DNA linear GSS 03-OCT-2000

DEFINITION 1M0226A14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0226A14 R, DNA sequence.

ACCESSION

AZ437960

VERSION

AZ437960.1

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingle, A., von Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

## TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss  
University of Utah  
Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0226 row: A column: 14  
Seq primer: CACACAGAAACAGCATATGACC  
Class: plasmid ends  
High quality sequence stop: 31.

## FEATURES

source

1. 31  
Location/Qualifiers

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0226A14"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## BASE COUNT

8 a 8 c 10 g 5 t

## ORIGIN

Query Match 74.3%; Score 10.4; DB 17; Length 31;  
Best Local Similarity 84.6%; Pred. No. 1.2e+05;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAGTCCAGNCCA 14  
|||||

DB 15 AAGTCCAGGCGCA 3

## RESULT 6

BI908094/C

LOCUS BI908094 46 bp mRNA linear EST 16-OCT-2001

DEFINITION 603067183F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5216252 5', mRNA sequence.

ACCESSION

BI908094

VERSION

BI908094.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be



Best Local Similarity 90.9%; Pred. No. 1.8e+05;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAGTCCAGNC 12  
11 AAGTCCAGNC 1

RESULT 9  
AA966941/c 34 bp mRNA linear EST 19-MAY-1998  
LOCUS u38c02.1 Soares\_mammary\_gland\_NbMNG Mus musculus cDNA clone  
DEFINITION IMAGE:1348994 5' similar to SW:ATPD\_PAT P35434 ATP SYNTHASE DELTA  
CHAIN: MITOCHONDRIAL PRECURSOR; mRNA sequence.

ACCESSION  
VERSION AA966941.1 GI:3140834  
KEYWORDS EST.

SOURCE  
ORGANISM

REFERENCE  
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMT Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMT Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:697786

Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28ml3 rev2 ET from Amersham  
High quality sequence stop: 1.

FEATURES  
source 1.34  
Location/Qualifiers

/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1348994"  
/clone\_id="Soares\_mammary\_gland\_NbMNG"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia)  
with a modified polylinker; Site.1: Not I; Site.2: Eco  
RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer [5',  
TGTTCACAACTCTGATGGAGCGCCGCGAGTGTCTTTTCTTTTCTTTTCTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
RNA provided by Dr. Minoru Ko, Wayne State Univ. library  
constructed and normalized by Bento Soares and M.Patima  
Bonaldo."

BASE COUNT 7 a 10 g 6 t  
ORIGIN 11 c

Query Match 71.4%; Score 10; DB 9; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCCAG 10

DB 23 CAAGTCCAG 14  
1111111111

RESULT 10  
BF036425/c 35 bp mRNA linear EST 20-OCT-2000  
LOCUS 60146045BF1 NIH\_MGC\_66 Homo sapiens cDNA clone IMAGE:3863775 5',  
DEFINITION mRNA sequence.

ACCESSION  
VERSION BF036425.1 GI:10744463  
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 35)

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@b-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://lmage.llnl.gov  
plate: LLM9604 row: d column: 16  
High quality sequence stop: 35.

FEATURES  
source 1.35  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3863775"  
/clone\_id="NIH\_MGC\_66"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: ovary; Vector: pCMV-SPORT6; Site.1: NotI;  
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.8 kb. Library constructed by Life  
Technologies."

BASE COUNT 9 a 9 c 12 g 5 t  
ORIGIN

Query Match 71.4%; Score 10; DB 12; Length 35;  
Best Local Similarity 90.9%; Pred. No. 2.1e+05;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGTCCAGNCCA 14  
31 GGTCCAGGCCA 21

RESULT 11  
T48919/c 42 bp mRNA linear EST 06-FEB-1995  
LOCUS yb07c07.s1 Stratiogene placenta (#937225) Homo sapiens cDNA clone  
DEFINITION IMAGE:70476 3' similar to similar to gb:M17885 60S ACIDIC RIBOSOMAL  
PROTEIN P0 (HUMAN), mRNA sequence.

ACCESSION  
VERSION T48919.1 GI:650779

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 42)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,  
Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins  
M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore  
B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,





TITLE Direct Submission  
JOURNAL Submitted (01-AUG-1996) Miki Ohira, Kazusa DNA Research Institute,  
Laboratory of Gene Structure 1: 1532-3 Yanaubino, Kisarazu, Chiba  
292, Japan (E-mail: oohira@kazusa.or.jp, Tel: +81-438-52-3932,  
Fax: +81-438-52-3931)

FEATURES  
Source  
1. 46  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="21"  
/map="21q22.2"  
/clone="E20-10"  
1. 46  
/note="trapped exon sequence"

BASE COUNT  
21 a 7 c 9 g 9 t

exon

Query Match 71.4%; Score 10; DB 17; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCCAG 10  
|||||  
17 CAAGTCCAG 8

Db

RESULT 14  
AUI02541 50 bp mRNA linear EST 30-AUG-2001  
LOCUS AUI02541  
DEFINITION AUI02541 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
HRC07574, mRNA sequence.  
ACCESSION AUI02541  
VERSION AUI02541.1 GI:13552062  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata  
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
JOURNAL 21270072  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
,S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1. 50  
/organism="Homo sapiens"  
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/clone="HRC07574"  
/clone\_11b="Sugano Homo sapiens cDNA library"  
/note="Differential display comparison of untreated and  
dimethylfumarate treated u937 cells"

BASE COUNT  
5 a 13 c 23 g 9 t

ORIGIN

Query Match 71.4%; Score 10; DB 9; Length 50;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGTCCAGNCCA 14  
|||||  
3 GGTCCAGTCCA 13

Db

RESULT 15  
AUI02547 50 bp mRNA linear EST 30-AUG-2001  
LOCUS AUI02547  
DEFINITION AUI02547 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
W1000, mRNA sequence.  
ACCESSION AUI02547  
VERSION AUI02547.1 GI:13552068  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata  
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki  
,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)  
JOURNAL 21270072  
COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano  
,S. Construction and characterization of a full length-enriched and  
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
Location/Qualifiers  
1. 50  
/organism="Homo sapiens"  
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/note="Differential display comparison of untreated and  
dimethylfumarate treated u937 cells"

BASE COUNT  
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ORIGIN

Query Match 71.4%; Score 10; DB 9; Length 50;  
Best Local Similarity 90.9%; Pred. No. 2.3e+05;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGTCCAGNCCA 14  
|||||  
1 GGTCCAGTCCA 11

Db

Search completed: June 21, 2003, 23:59:12  
Job time : 609.901 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 602.344 seconds  
(without alignments)  
1449.478 Million cell updates/sec

Title: US-09-964-666-9

Perfect score: 30

Sequence: 1 TTCAATCTGGTGAAGAGTGGACACCTGTG 30

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 841850

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:

1: gb\_da:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_cm:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pin:\*

35: em\_htg\_rod:\*

36: em\_htg\_mam:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_hcgo\_hum:\*

40: em\_hcgo\_mus:\*

41: em\_hcgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19.6	65.3	49	9	HUMD2H04M3	D17183 Human HepG2
2	15.8	52.7	31	6	AR051493	AR051493 Sequence
3	15.8	52.7	31	6	AR072633	AR072633 Sequence
4	15.8	52.7	31	6	AR073178	AR073178 Sequence
5	15.6	52.0	47	6	AX114379	AX114379 Sequence
6	15.4	51.3	29	6	AX411689	AX411689 Sequence
7	15.4	51.3	29	6	AX411691	AX411691 Sequence
8	15.2	50.7	38	6	AX056763	AX056763 Sequence
9	14.8	49.3	22	6	AX466859	AX466859 Sequence
10	14.8	49.3	31	6	AX247929	AX247929 Sequence
11	14.8	49.3	38	6	AX056759	AX056759 Sequence
12	14.8	49.3	39	6	I44807	I44807 Sequence 31
13	14.8	49.3	42	6	I44804	I44804 Sequence 28
14	14.8	49.3	50	10	AR071670	AR071670 Mus muscu
15	14.4	48.0	30	6	AX338660	AX338660 Sequence
16	14.2	47.3	36	6	E27466	E27466 Novel gene
17	14.2	47.3	39	6	AX044055	AX044055 Sequence
18	14.2	47.3	39	6	AX044109	AX044109 Sequence
19	14.2	47.3	39	6	AX044157	AX044157 Sequence
20	14.2	47.3	39	6	AX134391	AX134391 Sequence
21	14.2	47.3	40	6	AX068155	AX068155 Sequence
22	14.2	47.3	42	6	A93509	A93509 Sequence 12
23	14.2	47.3	48	6	A93513	A93513 Sequence 6
24	14.2	47.3	48	6	A93514	A93514 Sequence 7
25	14	46.7	24	6	AX290680	AX290680 Sequence
26	14	46.7	36	9	HUMTCVCVJ39	L39506 Homo sapien
27	14	46.7	36	9	HUMTCRDPAD	M64421 Human T cel
28	14	46.7	46	6	AR023959	AR023959 Sequence
29	14	46.7	46	6	I15460	I15460 Sequence 38
30	14	46.7	47	6	AX378324	AX378324 Sequence
31	14	46.7	47	6	AX378746	AX378746 Sequence
32	13.8	46.0	26	6	AR091186	AR091186 Sequence
33	13.8	46.0	26	6	AR198221	AR198221 Sequence
34	13.8	46.0	31	6	AX248794	AX248794 Sequence
35	13.8	46.0	35	6	E13897	E13897 PCR primer
36	13.8	46.0	43	6	A45335	A45335 Sequence 5
37	13.8	46.0	43	6	AR061140	AR061140 Sequence
38	13.8	46.0	43	9	HSARWG1A3	X75551 H.sapiens (
39	13.6	45.3	36	6	AX247486	AX247486 Sequence
40	13.4	44.7	24	6	A05412	A05412 Synthetic O
41	13.4	44.7	24	6	A09619	A09619 Oligonucleo
42	13.4	44.7	29	6	E13339	E13339 Probe. 4/19
43	13.4	44.7	40	6	AR059136	AR059136 Sequence
44	13.4	44.7	40	6	AR169562	AR169562 Sequence
45	13.4	44.7	50	6	AR032714	AR032714 Sequence

#### ALIGNMENTS

RESULT 1  
LOCUS HUMD2H04M3 49 bp mRNA linear PRI 04-FEB-1999  
DEFINITION Human HepG2 3' region Mbol cDNA, clone hmd2h04m3.  
ACCESSION D17183  
VERSION D17183.1 GI:598688  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens Male cell\_line:HepG2 cDNA to mRNA, clone\_hlb:Kisefu.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
AUTHORS Matoda,R., Okudo,K., Hori,N., Fukushima,A. and Matsubara,K.  
TITLE 1 (bases 1 to 49)  
The addition of 5'-coding information to a 3'-directed cDNA library  
Improves analysis of gene expression

Pred. No. is the number of results predicted by chance to have a

JOURNAL Gene 146 (2), 199-207 (1994)  
MEDLINE 94357437  
REFERENCE 2 (bases 1 to 49)  
AUTHORS Matoba,R.  
TITLE Direct Submission  
JOURNAL Submitted (21-JUL-1993) Ryo Matoba, Osaka University, Institute for Molecular and Cellular Bio; 1-3, Yamada-Oka, Suita, Osaka 565,  
Japan (E-mail:matoba@inherit.lnch.osaka-u.ac.jp,  
Tel:81-6-877-5111(x 3314). Fax:81-6-877-1922)  
COMMENT Submitted (21-JUL-1993) to DDBJ by:  
Ryo Matoba  
Molecular Microbiology and Genetics Lab.  
Research Institute of Innovative Technology for the Earth 9-2  
Kizugawada Kizu-cyo,  
Soraku-gun, Kyoto  
Japan, 619-02  
Phone: 07747-5-2308  
Fax: 07747-5-2321.  
Location/Qualifiers

FEATURES  
source 1..49  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/sex="Male"  
/cell\_line="HepG2"  
/clone\_1ib="Kiseru"

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Best Local Similarity 84.6%; Pred. No. 3.3e+02;  
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTCATCCTGGGTAAGTGGGACACC 26  
17 TTCACCTGGGCAAGAGTACACACC 42

RESULT 2  
AR051493/c  
LOCUS AR051493 31 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 63 from patent US 5830670.  
ACCESSION AR051493  
VERSION AR051493.1 GI:5974857  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 31)  
AUTHORS de la Monte,S. and Wands,J.R.  
TITLE Neural thread protein gene expression and detection of Alzheimer's disease  
JOURNAL Patent: US 5830670-A 63 03-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..31  
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BASE COUNT 6 a 10 c 8 g 7 t  
ORIGIN

Query Match 52.7%; Score 15.8; DB 6; Length 31;  
Best Local Similarity 74.1%; Pred. No. 2.1e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TTCATCCTGGGTAAGTGGGACACC 27  
27 TTCACCTGGGTAAGTGGGACACT 1

Db

RESULT 3  
AR072633/c  
LOCUS AR072633 31 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 63 from patent US 5948634.  
ACCESSION AR072633  
VERSION AR072633.1 GI:9999397

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 31)  
AUTHORS de la Monte,S. and Wands,J.R.  
TITLE Neural thread protein gene expression and detection of Alzheimer's disease  
JOURNAL Patent: US 5948634-A 63 07-SEP-1999;  
FEATURES Location/Qualifiers  
source 1..31  
/organism="unknown"

BASE COUNT 6 a 10 c 8 g 7 t  
ORIGIN

Query Match 52.7%; Score 15.8; DB 6; Length 31;  
Best Local Similarity 74.1%; Pred. No. 2.1e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TTCATCCTGGGTAAGTGGGACACC 27  
27 TTCACCTGGGTAAGTGGGACACT 1

Db

RESULT 4  
AR073178/c  
LOCUS AR073178 31 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 63 from patent US 5948888.  
ACCESSION AR073178  
VERSION AR073178.1 GI:9999941  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 31)  
AUTHORS de la Monte,S. and Wands,J.R.  
TITLE Neural thread protein gene expression and detection of Alzheimer's disease  
JOURNAL Patent: US 5948888-A 63 07-SEP-1999;  
FEATURES Location/Qualifiers  
source 1..31  
/organism="unknown"

BASE COUNT 6 a 10 c 8 g 7 t  
ORIGIN

Query Match 52.7%; Score 15.8; DB 6; Length 31;  
Best Local Similarity 74.1%; Pred. No. 2.1e+04;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TTCATCCTGGGTAAGTGGGACACC 27  
27 TTCACCTGGGTAAGTGGGACACT 1

Db

RESULT 5  
AX114379  
LOCUS AX114379 47 bp DNA linear PAT 11-MAY-2001  
DEFINITION Sequence 48 from Patent WO0129257.  
ACCESSION AX114379  
VERSION AX114379.1 GI:14031343  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 47)  
AUTHORS Schork,N. and Skierczynski,B.  
TITLE Methods of genetic cluster analysis and use thereof  
JOURNAL Patent: WO 0129257-A 48 26-APR-2001;  
GENSET (FR)  
FEATURES Location/Qualifiers  
source 1..47  
/organism="Homo sapiens"



[illegible]

SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 39)
AUTHORS	Pastan,I.H., Kreitman,R.J. and Puri,R.K.
TITLE	Fusion proteins comprising circularly permuted ligands
JOURNAL	Patent: US 5635599-A 31 03-JUN-1997;
FEATURES	location/Qualifiers
source	1..39
BASE COUNT	/organism="unknown"
ORIGIN	7 a 10 c 12 g 10 t
Query Match	49.3%: Score 14.8; DB 6; Length 39;
Best Local Similarity	73.1%: Pred. No. 6.1e+04;
Matches	19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY	2 TCATCTGGGTAAAGATGGGACACCT 27
Db	26 TCACCGGAGGTAAACGGTGGGACACT 1
RESULT 13	
LOCUS	144804 42 bp DNA Linear PAT 07-OCT-1997
DEFINITION	Sequence 28 from patent US 5635599.
ACCESSION	144804
VERSION	144804.1 GI:2469517
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 42)
AUTHORS	Pastan,I.H., Kreitman,R.J. and Puri,R.K.
TITLE	Fusion proteins comprising circularly permuted ligands
JOURNAL	Patent: US 5635599-A 28 03-JUN-1997;
FEATURES	location/Qualifiers
source	1..42
BASE COUNT	/organism="unknown"
ORIGIN	10 a 12 c 11 g 9 t
Query Match	49.3%: Score 14.8; DB 6; Length 42;
Best Local Similarity	73.1%: Pred. No. 6e+04; 7; Indels 0; Gaps 0;
Matches	19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY	2 TCATCTGGGTAAAGATGGGACACCT 27
Db	5 TCACCGGAGGTAAACGGTGGGACACT 30
RESULT 14	
LOCUS	AF071670 50 bp DNA linear ROD 26-JAN-1999
DEFINITION	Mus musculus clone MPJ-09 immunoglobulin heavy chain D-J region
ACCESSION	AF071670
VERSION	AF071670.1 GI:3320527
KEYWORDS	Mus musculus.
SOURCE	Mus musculus.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 50)
REFERENCE	Klonowski,K.D., Primiano,D.L. and Monestier,M.
AUTHORS	Atypical VH-D-JH rearrangements in newborn autoimmune MRL mice
TITLE	J. Immunol. 162 (3), 1566-1572 (1999)
JOURNAL	J. Immunol. 162 (3), 1566-1572 (1999)
MEDLINE	99138837
PUBMED	9973414
REFERENCE	2 (bases 1 to 50)
AUTHORS	Monestier,M. and Klonowski,K.
TITLE	Direct Submission
JOURNAL	Submitted (12-JUN-1998) Microbiology and Immunology, Temple



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OM nucleic acid search, using sw model

Run on: June 21, 2003, 21:23:51 ; Search time 164.531 Seconds  
(without alignments)  
410.621 Million cell updates/sec

Title: US-09-964-666-9

Perfect score: 30

Sequence: 1 TTCACTCGGTGGTAAGAGTGGACACCTCTG 30

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

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Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16.6	55.3	24	24	ABA05479
C 2	16.2	54.0	24	24	ABN89564
C 3	16	53.3	47	21	AAZ66299
C 4	16	53.3	47	22	AAE89248
C 5	16	53.3	50	16	AAZ25713
C 6	15.4	51.3	29	24	ABD31162
C 7	15.4	51.3	29	24	ABD31164
C 8	15.2	50.7	38	22	AAA91086
C 9	15.2	50.7	45	21	AAA28244

10	14.8	49.3	22	24	ABL92859	G protein-coupled
11	14.8	49.3	38	22	AAA91083	PCR primer flt1d2.
12	14.8	49.3	39	16	AAZ08201	Amplification prim
13	14.8	49.3	42	16	AAZ08198	Amplification prim
C 14	14.6	48.7	24	22	AAH76860	Human tyrosinase 1
C 15	14.6	48.7	33	21	AAA88764	Respiratory syncyt
C 16	14.6	48.7	45	21	AAA07136	S. pyogenes cystei
C 17	14.4	48.0	30	22	AAH27041	Interleukin 10 rec
C 18	14.4	48.0	47	21	AAZ69526	Human map-related
C 19	14.4	48.0	49	22	AAK65337	Human immune/haema
C 20	14.4	48.0	49	22	AAI62905	Human genomic DNA
C 21	14.2	47.3	36	20	AAZ88249	Human CRT-1 DNA pr
C 22	14.2	47.3	39	21	AAZ87155	Rice EBPSP PCR pri
C 23	14.2	47.3	39	21	AAZ88374	Primer G1. Synthe
C 24	14.2	47.3	39	21	AAZ88290	Human novel melast
C 25	14.2	47.3	39	22	AAZ03144	Chicken insulator
C 26	14.2	47.3	40	22	AAZ67684	Brassica sp. polym
C 27	14.2	47.3	41	19	AAV50841	Human glutamate re
C 28	14.2	47.3	41	19	AAV50842	Human glutamate re
C 29	14.2	47.3	41	24	ABO77609	Feline parvoviral
C 30	14.2	47.3	48	18	AAZ08795	Human cell divisio
C 31	14	46.7	24	24	ABK49469	Capture oligonucle
C 32	14	46.7	24	24	ABI87280	Capture oligonucle
C 33	14	46.7	24	24	ABI87281	Human tyrosinase 1
C 34	14	46.7	24	24	AAI69204	Human integrin beta-1 ch
C 35	14	46.7	27	19	AAV33786	PCR primer of the
C 36	14	46.7	27	19	AAV54819	M30 protein vector
C 37	14	46.7	28	24	AAI46529	Human alpha 2,3-si
C 38	14	46.7	41	24	ABI42407	Oligonucleotide pri
C 39	14	46.7	46	13	AAO24360	Human obesity-asso
C 40	14	46.7	47	24	ABK40865	Human USF2 gene bi
C 41	14	46.7	47	24	ABK41287	Human gene specifi
C 42	13.8	46.0	26	24	ABK67218	Human biallelic po
C 43	13.8	46.0	31	20	AAZ06222	Human single nucle
C 44	13.8	46.0	31	22	AAI30385	Human genomic EMBL
C 45	13.8	46.0	35	18	AAZ94899	

#### ALIGNMENTS

RESULT 1	
IDA ABA05479/c	
ABA05479 standard; DNA; 24 BP.	
XX	
AC ABA05479;	
XX	
01-MAR-2002 (first entry)	
XX	
DE Human RNA gyrase 12 PCR primer SEQ ID NO 4.	
XX	
KW Human: RNA gyrase 12; malignant tumour; haemopathy; HIV; infection;	
KW human immunodeficiency virus; immunological disease; inflammation;	
KW enzyme; PCR primer; ss.	
XX	
OS Homo sapiens.	
XX	
PN CNI311325-A.	
XX	
05-SEP-2001.	
XX	
02-MAR-2000: 2000CN-0111862.	
XX	
02-MAR-2000: 2000CN-0111862.	
XX	
02-MAR-2000: 2000CN-0111862.	
XX	
(BODE-) BODE GENE DEV CO LTD SHANGHAI.	
XX	
PI Mao Y, Xie Y;	
XX	
WPI: 2002-049927/07.	
DR	
XX	
PT New polypeptide-human RNA unwindase 12 and polynucleotide encoding the	
PT polypeptide -	

```
XX Example 2; Page 17 (Disclosure): 33pp; Chinese.
PS
CC This invention relates to human RNA gyrase 12, the polynucleotide encoding
CC this polypeptide and DNA recombinant techniques to produce this
CC polypeptide. The present invention also discloses a method of applying
CC this polypeptide to treat various diseases, such as malignant tumour,
CC haemopathy, HIV infection, immunological diseases and various
CC inflammations. The present sequence is that of a PCR primer, useful to
CC the invention.
XX
SQ Sequence 24 BP; 3 A; 10 C; 6 G; 5 T; 0 other:
Query Match 55.3%; Score 16.6; DB 24; Length 24;
Best Local Similarity 82.6%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 ATCTGGGTAAAGTGGACACC 26
DB 24 AGCTGGGTGAGAGTGAGACCCC 2
RESULT 2
ABN89564/c
ID ABN89564 standard; DNA; 24 BP.
XX
AC ABN89564;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human uracil mononucleotide synthetase 9.9 PCR primer 2 SEQ ID NO:4.
XX
KM Human; uracil mononucleotide synthetase 9.9; enzyme; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1333341-A.
XX
PD 30-JAN-2002.
XX
PF 07-JUL-2000; 2000CN-0117079.
XX
PR 07-JUL-2000; 2000CN-0117079.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI: 2002-340719/38.
XX
PT A human uracil mononucleotide synthetase 9.9 polypeptide, and the
XX polynucleotide encoding it, for treating various diseases -
XX
PS Example 2; Page 16 (Disclosure): 34pp; Chinese.
XX
CC The present invention describes human uracil mononucleotide synthetase
CC 9.9 (I). Also described is a process for producing (I) using DNA
CC recombination technology. (I) and the polynucleotide encoding it
CC can be used in the treatment of various diseases. The present sequence
CC represents a PCR primer for (I), which is used in an example from the
CC present invention.
XX
SQ Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 other:
Query Match 54.0%; Score 16.2; DB 24; Length 24;
Best Local Similarity 85.7%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 CCTGGTAGAGTGGACACC 26
DB 23 CCTGGCAGAGTGAAGACATCC 3
```

```
RESULT 3
AAZ66299
ID AAZ66299 standard; DNA; 47 BP.
XX
AC AAZ66299;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related diallelic marker SEQ ID NO:646.
XX
KM Human genome; diallelic marker: high density disequilibrium map;
KM genomic map; haplotype; phenotypic; polymorphic base; genotyping;
KM haplotyping; hybridisation; identification; characterisation;
KM diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,C)
FT /*tag=
FT /standard_name="single nucleotide polymorphism"
XX
PN WO954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
XX
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST ) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI: 2000-013267/01.
XX
PT Novel diallelic markers used to construct a high density disequilibrium
XX map of the human genome -
XX
PS Claim 1; Page 368; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human diallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ6579 to AAZ77440 represent amplification
CC primers for the diallelic markers. The diallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 16 A; 14 C; 8 G; 9 T; 0 other:
Query Match 53.3%; Score 16; DB 21; Length 47;
Best Local Similarity 79.2%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CATCTGGCTAAGAGTGGACACC 26
DB 10 CATCTGGCTAAGAGTGAACAC 33
RESULT 4
AAF89248
ID AAF89248 standard; DNA; 47 BP.
```

XX AAF89248;  
AC 10-DEC-2001 (first entry)  
XX  
DE Sample member clustering method related human polymorphic site #48.  
XX  
XX Cluster: hierarchical clustering algorithm; population based study;  
KM clinical trial: DNA fingerprint; genetic profile analysis; PCR primer;  
KM SNP; single nucleotide polymorphism; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key location/Qualifiers  
FT allele replace(24,C)  
FT /tag- a  
XX  
PN WO200129257-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 20-OCT-2000; 2000WO-IB01632.  
XX  
PR 22-OCT-1999; 99GS-0161231.  
PR 07-JUL-2000; 2000US-0216897.  
XX  
PA (GEST ) GENSET.  
XX  
PI Schork N, Skierczynski B;  
XX  
DR WPI: 2001-316248/33.  
XX  
PT Genetic clustering by distributing members into optimal numbers of  
PT clusters determined by a hierarchical clustering algorithm or by  
PT paired-pair analysis of homozygous pairs in clusters got from  
PT non-hierarchical clustering -  
XX  
PS Claim 61; Page 71; 100pp; English.  
XX  
CC The present invention describes methods of clustering members of a  
CC sample, involving applying a hierarchical clustering algorithm to the  
CC sample members, determining the optimal number of clusters based on this  
CC and distributing the sample members into clusters using non-hierarchical  
CC clustering. The methods are useful in population based studies such as  
CC clinical trials, DNA fingerprinting and genetic profile analyses. The  
CC present sequence was used to demonstrate the method of the invention.  
XX  
SQ Sequence 47 BP; 16 A; 14 C; 8 G; 9 T; 0 other;  
XX  
Query Match 53.3%; Score 16; DB 22; Length 47;  
Best Local Similarity 79.2%; Pred. No. 8.9e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
XX  
QY 3 CATCCTGGGTAAGAGTGACAC 26  
DB 10 CATCCTGGGTAAGAGTGACAC 33  
XX  
RESULT 5  
AAT25713  
ID AAT25713 standard; CDNA to mRNA; 50 BP.  
XX  
AC AAT25713;  
XX  
DT 10-OCT-1996 (first entry)  
XX  
DE Human gene signature HUMGS07919.  
XX  
KM Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
KM human; cloning; mapping; non-biased library; diagnosis; detection;  
KM cell typing; abnormal cell function; ss.  
XX  
OS Homo sapiens.

XX MO9514772-A1.  
PN 01-JUN-1995.  
XX  
PD 11-NOV-1994; 94WO-JF01916.  
XX  
PF 12-NOV-1993; 93JP-0355504.  
XX  
PR (MATS/) MATSUBARA K.  
XX (OKUBO/) OKUBO K.  
XX  
PA Matsubara K, Okubo K;  
PI WPI: 1995-206931/27.  
XX  
DR Identifying gene signatures in 3'-directed human cDNA library - e.g.  
XX for diagnosis of abnormal cell function, by preparing cDNA that  
XX reflects relative abundance of corresp. mRNA in specific human  
XX tissues  
XX  
PS Claim 1; Page 1912; 2245pp; Japanese.  
XX  
CC A single-stranded DNA (or its complementary strand or the corresp.  
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences  
CC given in AAT19001-T26837 and which is able to hybridise to part of  
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)  
CC sequences were obtained from 3'-directed cDNA libraries prepared  
CC from various human tissues; synthesis of cDNA was initiated from the  
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-  
CC untranslated sequence is unique to a particular mRNA species, almost  
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library  
CC is constructed so as to reflect accurately the relative abundance of  
CC different mRNAs in the particular tissue from which it was derived.  
CC The appearance frequency of a given GS in a cDNA library can be  
CC determined (esp. using primers and probes derived from the GS  
CC sequences) as a means of diagnosing abnormal cell function or for  
CC recognising different cell types.  
XX  
SQ Sequence 50 BP; 12 A; 13 C; 12 G; 12 T; 1 other;  
XX  
Query Match 53.3%; Score 16; DB 16; Length 50;  
Best Local Similarity 76.0%; Pred. No. 8.9e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
XX  
QY 1 TTCATCCTGGGTAAGAGTGACAC 25  
DB 17 TCCAGNCTGGCTAACAGTCGACTC 41  
XX  
RESULT 6  
AAD31162/c  
ID AAD31162 standard; DNA; 29 BP.  
XX  
AC AAD31162;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE Primer IP14924 for cloning human IGS43 GPCR cDNA.  
XX  
IGS43: G-protein coupled receptor; GPCR; uterus; lung; trachea;  
KM colon; small intestine; stomach; mammary gland; prostate; testis;  
KM psychiatric disorder; central nervous system disorder; schizophrenia;  
KM episodic and paroxysmal anxiety disorder; Parkinson's disease;  
KM multiple sclerosis; Alzheimer's disease; cardiovascular disease;  
KM heart failure; angina pectoris; kidney disease; dyslipidaemias; obesity;  
KM emesis; gastrointestinal disorder; inflammatory bowel disease; diabetes;  
KM osteoporosis; inflammation; infection; human immunodeficiency virus; HIV;  
KM cancer; immune disorder; urinary retention; asthma; allergy; arthritis;  
KM benign prostatic hypertrophy; endotoxin shock; sepsis; gene therapy;  
KM gynaecological disorder; vaccine; human; PCR primer; ss.  
XX  
OS Homo sapiens.

XX WO200228897-A2.  
 XX 11-APR-2002.  
 XX 28-SEP-2001; 2001WO-EP11319.  
 XX 02-OCT-2000; 2000EP-0203411.  
 XX 04-OCT-2000; 2000US-237394P.  
 XX (SOLV ) SOLVAY PHARM BV.  
 XX Deleersnijder W, Blockx H, De Moor L;  
 XX WPI; 2002-426102/45.  
 XX Novel G-protein coupled receptor, termed IGS43 polypeptide and nucleic  
 PT acid encoding the polypeptide, useful for treating disorders of uterus,  
 PT kidney, lung, colon, stomach, mammary gland, prostate and testis -  
 XX Example 1; Page 33; 59pp; English.

CC The invention relates to IGS43 G-protein coupled receptor (GPCR) and the  
 CC polynucleotide encoding it. The IGS43 polypeptide, polynucleotide,  
 CC agonist, antagonist or antibody is useful for treating dysfunctions or  
 CC disorders related to uterus, kidney, lung, trachea, colon, small  
 CC intestine, stomach, mammary gland, prostate, testis, central nervous  
 CC system, cerebellum and spinal cord. The polypeptide is useful as vaccine  
 CC for inducing immunological response in a mammal, for treating  
 CC psychiatric and central nervous system disorders including  
 CC schizophrenia, episodic and paroxysmal anxiety disorders e.g. obsessive  
 CC compulsive disorder, post traumatic disorder, phobia and panic, major  
 CC depressive disorder, bipolar disorder, Parkinson's disease, general  
 CC anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer's  
 CC disease, dementia, severe mental retardation, Huntington's disease,  
 CC dyskinesias, Tourette's syndrome, tics, tremor, dystonia, spasms,  
 CC anorexia, bulimia, stroke, addiction/dependency/craving, sleep  
 CC disorder, epilepsy, migraine, attention deficit/hyperactivity disorder,  
 CC cardiovascular diseases including heart failure, angina pectoris,  
 CC arrhythmias, myocardial infarction, cardiac hypertrophy, hypertension,  
 CC hypertension, thrombosis, arteriosclerosis, cerebral vasospasm,  
 CC subarachnoid haemorrhage, cerebral ischaemia, cerebral infarction,  
 CC peripheral vascular disease, Raynaud's disease, kidney disease,  
 CC dyslipidaemias, obesity, emesis, gastrointestinal disorders including  
 CC irritable bowel syndrome, inflammatory bowel disease, diabetic  
 CC gastroparesis and diabetes, ulcers, diarrhoea, osteoporosis,  
 CC inflammations, infections including bacterial, fungal, protozoan and  
 CC viral infections, particularly human immunodeficiency virus (HIV)-1 or  
 CC HIV-2 infections, pain, cancers, chemotherapy induced injury, tumour  
 CC invasion, immune disorders, urinary retention, asthma, allergies,  
 CC arthritis, benign prostatic hypertrophy, endotoxin shock, sepsis,  
 CC complications of diabetes mellitus, and gynaecological disorders.  
 CC The polypeptide and polynucleotide of the invention are also useful as  
 CC research reagents and materials for discovery of treatments and  
 CC diagnostics to animal and human diseases. The polynucleotide is  
 CC also useful for chromosome identification. The polypeptide is also useful  
 CC for assessing the binding of small molecule substrates and ligands in  
 CC cells, cell-free preparations, chemical libraries and natural product  
 CC mixtures. The present sequence is a PCR primer used for cloning human  
 CC IGS43 GPCR cDNA.

XX Sequence 29 BP; 5 A; 10 C; 6 G; 8 T; 0 other:

Query Match 51.3% Score 15.4; DB 24; Length 29;  
 Best Local Similarity 94.1%; Pred. No. 1.6e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 AGAGTGGACACCTGTG 30  
 ||||| ||||| ||||| |||||  
 DB 27 AGAGAGGACACCTGTG 11

Result 7

AAD31164/C  
 ID AAD31164 standard; DNA; 29 BP.  
 XX AAD31164;  
 XX 27-AUG-2002 (first entry)  
 XX Human IGS43 GPCR DNA amplifying primer IP15332.  
 XX IGS43; G-protein coupled receptor; GPCR; uterus; lung; trachea;  
 KW colon; small intestine; stomach; mammary gland; prostate; testis;  
 KW psychiatric disorder; central nervous system disorder; schizophrenia;  
 KW episodic and paroxysmal anxiety disorder; Parkinson's disease;  
 KW multiple sclerosis; Alzheimer's disease; cardiovascular disease;  
 KW heart failure; angina pectoris; kidney disease; dyslipidaemias; obesity;  
 KW emesis; gastrointestinal disorder; inflammatory bowel disease; diabetes;  
 KW osteoporosis; inflammation; infection; human immunodeficiency virus; HIV;  
 KW cancer; immune disorder; urinary retention; asthma; allergy; arthritis;  
 KW benign prostatic hypertrophy; endotoxin shock; sepsis; gene therapy;  
 KW gynaecological disorder; vaccine; human; PCR primer; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200228897-A2.  
 XX 11-APR-2002.  
 XX 28-SEP-2001; 2001WO-EP11319.  
 XX 02-OCT-2000; 2000EP-0203411.  
 XX 04-OCT-2000; 2000US-237394P.  
 XX (SOLV ) SOLVAY PHARM BV.  
 XX Deleersnijder W, Blockx H, De Moor L;  
 XX WPI; 2002-426102/45.  
 XX Novel G-protein coupled receptor, termed IGS43 polypeptide and nucleic  
 PT acid encoding the polypeptide, useful for treating disorders of uterus,  
 PT kidney, lung, colon, stomach, mammary gland, prostate and testis -  
 XX Example 2; Page 36; 59pp; English.

CC The invention relates to IGS43 G-protein coupled receptor (GPCR) and the  
 CC polynucleotide encoding it. The IGS43 polypeptide, polynucleotide,  
 CC agonist, antagonist or antibody is useful for treating dysfunctions or  
 CC disorders related to uterus, kidney, lung, trachea, colon, small  
 CC intestine, stomach, mammary gland, prostate, testis, central nervous  
 CC system, cerebellum and spinal cord. The polypeptide is useful as vaccine  
 CC for inducing immunological response in a mammal, for treating  
 CC psychiatric and central nervous system disorders including  
 CC schizophrenia, episodic and paroxysmal anxiety disorders e.g. obsessive  
 CC compulsive disorder, post traumatic disorder, phobia and panic, major  
 CC depressive disorder, bipolar disorder, Parkinson's disease, general  
 CC anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer's  
 CC disease, dementia, severe mental retardation, Huntington's disease,  
 CC dyskinesias, Tourette's syndrome, tics, tremor, dystonia, spasms,  
 CC anorexia, bulimia, stroke, addiction/dependency/craving, sleep  
 CC disorder, epilepsy, migraine, attention deficit/hyperactivity disorder,  
 CC cardiovascular diseases including heart failure, angina pectoris,  
 CC arrhythmias, myocardial infarction, cardiac hypertrophy, hypertension,  
 CC hypertension, thrombosis, arteriosclerosis, cerebral vasospasm,  
 CC subarachnoid haemorrhage, cerebral ischaemia, cerebral infarction,  
 CC peripheral vascular disease, Raynaud's disease, kidney disease,  
 CC dyslipidaemias, obesity, emesis, gastrointestinal disorders including  
 CC irritable bowel syndrome, inflammatory bowel disease, diabetic  
 CC gastroparesis and diabetes, ulcers, diarrhoea, osteoporosis,  
 CC inflammations, infections including bacterial, fungal, protozoan and  
 CC viral infections, particularly human immunodeficiency virus (HIV)-1 or  
 CC HIV-2 infections, pain, cancers, chemotherapy induced injury, tumour  
 CC invasion, immune disorders, urinary retention, asthma, allergies,  
 CC arthritis, benign prostatic hypertrophy, endotoxin shock, sepsis,

CC complications of diabetes mellitus, and gynaecological disorders.  
CC The polypeptide and polynucleotide of the invention are also useful as  
CC research reagents and materials for discovery of treatments and  
CC diagnostics to animal and human diseases. The polynucleotide is  
CC also useful for chromosome identification. The polypeptide is also useful  
CC for assessing the binding of small molecule substrates and ligands in  
CC cells, cell-free preparations, chemical libraries and natural product  
CC mixtures. The present sequence is a PCR primer used for amplifying human  
CC IGSA3 GPCR DNA.

CC Sequence 29 BP; 4 A; 10 C; 8 G; 7 T; 0 other;

Query Match 51.3%; Score 15.4; DB 24; Length 29;  
Best Local Similarity 94.1%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 AGAGTGGGACACCTGTG 30  
DB 27 AGAGAGGGACACCTGTG 11

# RESULT 8

AAA91086/C  
ID AAA91086 standard; DNA; 38 BP.

AC AAA91086;

DT 05-APR-2001; (first entry)

DE PCR primer F11D2.VEGFR3D3.s for F11l receptor fusion DNA sequence.

KW F11l receptor; fusion protein; chimeric protein; pharmacokinetic;  
KW plasma leakage; vascular permeability; IgG Fc region; PCR primer; ss.

OS Unidentified.

PN WO200075319-A1.

PD 14-DEC-2000;

PF 23-MAY-2000; 2000WO-US14142.

PR 08-JUN-1999; 99US-0138133.

PA (REGG-) REGENERON PHARM INC.

PI Papadopoulos NJ, Davis S, Yancopoulos GD;

DR WPI; 2001-071076/08.

PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
PT and its fragments, useful for diagnosis, evaluation, and treatment of  
PT diseases associated with the gene expression and for producing model  
PT systems -

Example 17; Page 63; 159pp; English.

CC This sequence represents a PCR primer used to construct DNA  
CC sequences encoding the fusion proteins of the invention between  
CC the F11l receptor and the Fc region of IgG. The specification relates  
CC to modified chimeric polypeptides with improved pharmacokinetics. The  
CC modified chimeric polypeptides are preferably F11l receptor polypeptides  
CC that have been modified to improve their pharmacokinetic profile. The  
CC polypeptides can be used to decrease or inhibit plasma leakage and/or  
CC vascular permeability in a mammal.

CC Sequence 38 BP; 9 A; 9 C; 11 G; 9 T; 0 other;

Query Match 50.7%; Score 15.2; DB 22; Length 38;  
Best Local Similarity 71.4%; Pred. No. 2e+03;  
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CATCTGGGTAGTGGACACCTGTG 30

DB 29 CTTCCTGGGACACAGCTGATATCTATG 2

RESULT 9  
AAA28244/C  
ID AAA28244 standard; DNA; 45 BP.

AC AAA28244;

DT 12-FEB-2001 (first entry)

DE Upstream45 primer used in the construction of mutant YJR012C gene.

KW Essential gene identification; antifungal agent; yeast; germination;  
KW growth; pseudohyphal growth; hyphal growth; proliferation; insecticide;  
KW herbicide; PCR primer; YJR012C; ss.

OS Saccharomyces cerevisiae.

PN WO200058457-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US08641.

PR 31-MAR-1999; 99US-0127272.

PA (ROSE-) ROSETTA INPHARMATICS INC.

PI Dimster-Denk DF;

DR WPI; 2000-594641/56.

PT Identifying a target gene for design or discovery of an antifungal  
PT agent, insecticide, or herbicide, comprising disrupting the function of  
PT a gene in a yeast cell and identifying whether the function is  
PT essential for e.g. germination -

Example 3; Fig 15; 156pp; English.

CC This invention relates to a method for the identification of a target  
CC gene useful for the design or discovery of an antifungal agent. The  
CC method comprises disrupting the function of a gene in a yeast cell, and  
CC identifying whether the function is essential for germination, growth,  
CC pseudohyphal growth or hyphal growth. The invention further comprises  
CC determining whether the protein encoded by the essential gene has  
CC homology to a mammalian, plant or insect protein. The methods are useful  
CC for identifying genes in Saccharomyces cerevisiae which are essential for  
CC germination and proliferation of S. cerevisiae and using the identified  
CC genes or their encoded proteins as targets for highly specific antifungal  
CC agents, insecticides, herbicides and antiproliferation drugs. The  
CC invention includes examples of the use of the method, comprising the  
CC formation and characterisation of a number of S. cerevisiae genes to  
CC determine if they are essential for growth of the yeast. The present  
CC sequence represents a PCR primer used in the construction and analysis of  
CC the S. cerevisiae YJR012C mutant strain.

CC Sequence 45 BP; 20 A; 10 C; 7 G; 8 T; 0 other;

Query Match 50.7%; Score 15.2; DB 21; Length 45;  
Best Local Similarity 85.0%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CATCTGGGTAGTGGGA 22  
DB 45 CATCTTGGTGGTAGAGTCGGA 26

RESULT 10  
ABL92859  
ID ABL92859 standard; DNA; 22 BP.

XX

AC ABL92859;  
 XX  
 DT 06-JUN-2002 (first entry)  
 XX  
 DE G protein-coupled receptor GPCR10 PCR primer SEQ ID NO:341.  
 XX  
 KW Human: G protein-coupled receptor; antidiabetic; anorectic; cytostatic;  
 KW Immunomodulator; neuroprotective; nootropic; antiparkinsonian; metabolic;  
 KW immunosuppressive; ophthalmological; antibacterial; vitrucoe; fungicide;  
 KW protozoacide; hypertensive; hypotensive; analgesic; osteopathic;  
 KW antitumor; antitasthmatic; antiallergic; anti-HIV; antilipemic; vaccine;  
 KW antifertility; antinflammatory; haemostatic; cell signal processing;  
 KW cardiomyopathy; atherosclerosis; metabolic pathway modulation; cancer;  
 KW gene therapy; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200212343-A2.  
 XX  
 PD 14-FEB-2002.  
 XX  
 PF 07-AUG-2001: 2001WO-US24787.  
 XX  
 PR 07-AUG-2000: 2000US-223138P.  
 PR 07-AUG-2000: 2000US-223472P.  
 PR 11-AUG-2000: 2000US-224613P.  
 PR 11-AUG-2000: 2000US-224815P.  
 PR 05-JAN-2001: 2001US-260003P.  
 PR 05-JAN-2001: 2001US-260072P.  
 PR 08-JAN-2001: 2001US-260283P.  
 PR 09-JAN-2001: 2001US-260450P.  
 PR 10-JAN-2001: 2001US-261156P.  
 PR 22-JAN-2001: 2001US-263338P.  
 PR 23-JAN-2001: 2001US-263434P.  
 PR 01-FEB-2001: 2001US-265704P.  
 PR 20-FEB-2001: 2001US-269964P.  
 PR 09-MAR-2001: 2001US-274873P.  
 PR 15-MAR-2001: 2001US-276406P.  
 PR 01-MAY-2001: 2001US-287916P.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX  
 PI Spytek KA, Padigaru M, Zernhusen BD, Baumgartner JC, Li L;  
 PI Casman SJ, Vernet CAM, Ballinger RA, Shenoy SG, Kekuda R;  
 PI Bureses CE, Mezes PS, Grosse WM, Alsobrook JP, Gorman L;  
 PI Larochele WJ, Taupier RJ, Colman SD, Szekeres ES;  
 XX  
 DR WPI: 2002-217180/27.  
 XX  
 PT New G-protein coupled receptor polypeptides and nucleic acids, useful  
 PT for diagnosis, prevention or treatment of hematopoietic,  
 PT neurodegenerative, immune and signal transduction pathway disorders -  
 XX  
 XX Example 2; Page 357; 492pp; English.  
 PS  
 CC The present invention describes novel human G protein-coupled receptors  
 CC (GPCR) designated GPCR1-36 from the present invention. The GPCRs can have  
 CC activities such as: antidiabetic; anorectic; immunomodulator; cytostatic;  
 CC neuroprotective; nootropic; antiparkinsonian; analgesic; osteopathic;  
 CC immunosuppressive; metabolic; ophthalmological; antibacterial; vitrucoe;  
 CC fungicide; protozoacide; hypertensive; hypotensive; anti-HIV; antitumor;  
 CC antitasthmatic; antilipemic; antiallergic; antifertility; haemostatic;  
 CC and antinflammatory. They can be used in gene therapy and vaccine  
 CC production. The GPCR proteins can be used for treating or preventing  
 CC GPCR-associated disorders such as cardiomyopathy, atherosclerosis, or a  
 CC disorder related to cell signal processing and metabolic pathway  
 CC modulation. In humans, GPCR proteins and the polynucleotides encoding  
 CC them are useful for determining the presence of or predisposition to a  
 CC disease, especially cancer associated with altered levels of GPCR  
 CC proteins and polynucleotides, by measuring the level of protein  
 CC expression or the amount of nucleic acid from a mammal and comparing it  
 CC with another mammal not having or not predisposed to the disease. GPCR  
 CC proteins are also useful for identifying an agent, especially cellular

CC receptor or a downstream effector that binds to GPCR, for screening of a  
 CC candidate substance interacting with an olfactory receptor polypeptide,  
 CC its fragments or variants. The present sequence represents a PCR primer  
 CC used in the isolation of a novel human GPCR in the present invention.  
 XX  
 XX Sequence 22 BP; 7 A; 5 C; 6 G; 4 T; 0 other;

Query Match 49.3%; Score 14.8; DB 24; Length 22;  
 Best Local Similarity 88.9%; Pred. No. 2.8e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 CATCCTGGGTAAAGATGG 20  
 |||||  
 DB 5 CATCCTGGGTAAAGAAAG 22

RESULT 11  
 AAA91083  
 ID AAA91083 standard; DNA; 38 BP.  
 XX  
 AC AAA91083;  
 XX  
 DT 05-APR-2001 (first entry)  
 XX  
 DE PCR primer F11D2.VEGFR3D3.as for F11 receptor fusion DNA sequence.  
 XX  
 KW F11 receptor; fusion protein; chimeric protein; pharmacokinetic;  
 KW plasma leakage; vascular permeability; IgG Fc region; PCR primer; ss.  
 XX  
 OS unidentified.  
 OS  
 PN WO200075319-A1.  
 XX  
 PD 14-DEC-2000.  
 XX  
 PE 23-MAY-2000: 2000WO-US14142.  
 XX  
 PR 08-JUN-1999: 99US-0138133.  
 XX  
 XX (REG-) REGENERON PHARM INC.  
 PA  
 XX  
 PI Papadopoulos NJ, Davis S, Yancopoulos GD;  
 PI WPI: 2001-071076/08.  
 DR  
 XX  
 PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
 PT and its fragments, useful for diagnosis, evaluation, and treatment of  
 PT diseases associated with the gene expression and for producing model  
 PT systems -  
 XX  
 PS Example 17; Page 62; 159pp; English.  
 XX  
 CC This sequence represents a PCR primer used to construct DNA  
 CC sequences encoding the fusion proteins of the invention between  
 CC the F11 receptor and the Fc region of IgG. The specification relates  
 CC to modified chimeric polypeptides with improved pharmacokinetics. The  
 CC modified chimeric polypeptides are preferably F11 receptor polypeptides  
 CC that have been modified to improve their pharmacokinetic profile. The  
 CC polypeptides can be used to decrease or inhibit plasma leakage and/or  
 CC vascular permeability in a mammal.  
 XX  
 SQ Sequence 38 BP; 8 A; 6 C; 10 G; 14 T; 0 other;

Query Match 49.3%; Score 14.8; DB 22; Length 38;  
 Best Local Similarity 73.1%; Pred. No. 3e+03; 7; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 5 TCCTGGGTAAAGATGGACACCTGG 30  
 |||||  
 DB 2 TCCTGGGTAAAGATGGATATCTATG 27

RESULT 12

AA08201/c  
ID AA08201 standard; DNA: 39 BP.  
XX  
AC AA08201:  
XX  
DT 28-MAY-1996 (first entry)  
XX  
DE Amplification primer BK138.  
XX  
KW Linker: Interleukin-4; Interleukin-2; IL-4; IL-2; G-CSF; GM-CSF;  
KW granulocyte-colony stimulating factor; circularly permuted ligand;  
KW cancer; therapy; granulocyte macrophage-colony stimulating factor;  
KW polymerase chain reaction; PCR; primer; amplify; ss.  
XX  
OS Synthetic.  
XX  
PN WO9527732-A2.  
XX  
PD 19-OCT-1995.  
XX  
PF 06-APR-1995; 95WO-US04468.  
XX  
PR 08-APR-1994; 94US-0225224.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Kreitman RJ, Pastan I;  
XX  
DR WPI: 1995-366354/47.  
XX  
PT Circularly permuted ligands and chimeric mols. are modified  
PT Interleukin(s) or colony-stimulating factors - with increased  
PT binding specificity and affinity for inhibiting tumours  
XX  
PS Example 5; Page 35; 97pp; English.  
XX  
CC AA08176-T08219 represent amplification primers used in the construction  
CC of modified ligands. The modified ligands comprise two copies of a  
CC sequence joined to a linker. The sequences used in the ligand include  
CC Interleukin-4 (IL-4), IL-2, granulocyte-colony stimulating factor  
CC (G-CSF) and granulocyte macrophage-colony stimulating factor (GM-CSF).  
CC The linker regions used are represented by AAR87726 and AAR87730. This  
CC sequence was used in conjunction with AA08200 to amplify codons 39-127  
CC of IL-2 for use in a modified ligand. These modified ligands are known  
CC as circularly permuted ligands. The modified ligands can be joined to  
CC another protein (preferably a cytotoxin or an antibody) using a spacer  
CC (see AAR87732-R87734). The circularly permuted ligands have greater  
CC specificity and binding affinity than the original ligand. They can be  
CC used in chimeric molecules to inhibit the growth of tumour cells in vivo,  
CC where the two copies of the protein sequence are joined to cytotoxins.  
XX  
SO Sequence 39 BP; 7 A; 10 C; 12 G; 10 T; 0 other;  
Query Match 49.3%; Score 14.8; DB 16; Length 39;  
Best Local Similarity 73.1%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
OY 2 TCATCTGGGTAAAGTGGGACACT 27  
DB 26 TCACCGAGGTAAAGTGGGACACT 1  
RESULT 13  
AA08198  
ID AA08198 standard; DNA: 42 BP.  
XX  
AC AA08198:  
XX  
DT 28-MAY-1996 (first entry)  
XX  
DE Amplification primer BK135.  
XX  
KW Linker: Interleukin-4; Interleukin-2; IL-4; IL-2; G-CSF; GM-CSF;

KW granulocyte-colony stimulating factor; circularly permuted ligand;  
KW cancer; therapy; granulocyte macrophage-colony stimulating factor;  
KW polymerase chain reaction; PCR; primer; amplify; ss.  
XX  
OS Synthetic.  
XX  
PN WO9527732-A2.  
XX  
PD 19-OCT-1995.  
XX  
PF 06-APR-1995; 95WO-US04468.  
XX  
PR 08-APR-1994; 94US-0225224.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Kreitman RJ, Pastan I;  
XX  
DR WPI: 1995-366354/47.  
XX  
PT Circularly permuted ligands and chimeric mols. are modified  
PT Interleukin(s) or colony-stimulating factors - with increased  
PT binding specificity and affinity for inhibiting tumours  
XX  
PS Example 5; Page 35; 97pp; English.  
XX  
CC AA08176-T08219 represent amplification primers used in the construction  
CC of modified ligands. The modified ligands comprise two copies of a  
CC sequence joined to a linker. The sequences used in the ligand include  
CC Interleukin-4 (IL-4), IL-2, granulocyte-colony stimulating factor  
CC (G-CSF) and granulocyte macrophage-colony stimulating factor (GM-CSF).  
CC The linker regions used are represented by AAR87726 and AAR87730. This  
CC sequence was used in conjunction with AA08199 to amplify a codons 1-38  
CC of IL-2 for use in a modified ligand. These modified ligands are known  
CC as circularly permuted ligands. The modified ligands can be joined to  
CC another protein (preferably a cytotoxin or an antibody) using a spacer  
CC (see AAR87732-R87734). The circularly permuted ligands have greater  
CC specificity and binding affinity than the original ligand. They can be  
CC used in chimeric molecules to inhibit the growth of tumour cells in vivo,  
CC where the two copies of the protein sequence are joined to cytotoxins;  
XX  
SO Sequence 42 BP; 10 A; 12 C; 11 G; 9 T; 0 other;  
Query Match 49.3%; Score 14.8; DB 16; Length 42;  
Best Local Similarity 73.1%; Pred. No. 3.1e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
OY 2 TCATCTGGGTAAAGTGGGACACT 27  
DB 5 TCACCGAGGTAAAGTGGGACACT 30  
RESULT 14  
AAH76860/c  
ID AAH76860 standard; DNA: 24 BP.  
XX  
AC AAH76860:  
XX  
DT 14-DEC-2001 (first entry)  
XX  
DE Human tyrosinase 15 RT-PCR primer, SEQ ID NO:4.  
XX  
KW Human: tyrosinase 15; recombinant production;  
KW malignant tumour; cancer; blood disease; HIV infection;  
KW human immunodeficiency virus; immune disorder; inflammatory condition;  
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator;  
KW reverse transcription-PCR; RT-PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200171001-A1.  
XX  
PD 27-SEP-2001.

```
XX 19-MAR-2001; 2001WO-CN00357.
PF
XX
XX 22-MAR-2000; 2000CN-0115044.
PR
XX
XX (BIOW-) BIOWINDOM GENE DEV INC SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI: 2001-602790/68.
DR
XX
XX Human tyrosinase 15 and encoded polynucleotide, used in diagnosis and
PT treatment of malignant tumors, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and inflammation -
PS
XX
XX Example 2; Page 11; 33pp; Chinese.
PS
XX
XX The invention relates to human tyrosinase 15 (AA66766), nucleic acids
CC encoding it (AAH76858), and a method for the recombinant production of
CC tyrosinase 15. The protein has a molecular weight of 15 kD. The present
CC invention additionally discloses an antagonist of tyrosinase 15 for
CC therapeutic use, and an antibody which specifically binds to tyrosinase
CC 15. Tyrosinase 15, and nucleotides which encode it may be used for
CC treating a variety of diseases, such as malignant tumours, blood
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC and inflammatory conditions. The protein may also be used to screen for
CC modulators of its activity or for peptide fingerprinting identification.
CC The polynucleotide can be used as a primer for nucleic acid amplification
CC reactions or as a probe for hybridisation reactions, or in producing gene
CC chips or microarrays. Sequences AAH76859-AAH76860 represent reverse
CC transcription-PCR (RT-PCR) primers used in an exemplification of the
CC invention to isolate human tyrosinase 15 cDNA.
XX
SQ Sequence 24 BP; 3 A; 9 C; 8 G; 4 T; 0 other;
Query Match 48.7%; Score 14.6; DB 22; Length 24;
Best Local Similarity 81.0%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6 CCTGGGTAGAGTGGGACAC 26
DB 23 CCTGGGTAGAGTGGGACAC 3
RESULT 15
AAA88764
ID AAA88764 standard; DNA; 33 BP.
XX
XX AAA88764;
AC
XX
XX 19-FEB-2001 (first entry)
DT
XX
XX Respiratory syncytial virus NS1-NS2 gene fusion region.
DE
XX
XX RSV; vaccine; attenuation; pneumonia; bronchiolitis; NS1 gene;
KM NS2 gene; mutant; ss.
XX
XX Human respiratory syncytial virus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 1..23
FT 5'UTR
FT /*tag= a
FT /note= "NS1 nontranslated region"
FT CDS 24..35
FT /*tag= b
FT /partial
FT /note= "5' end of NS2 open reading frame"
XX
XX WO200061611-A2.
XX
XX 19-QCR-2000.
XX
```

```
PF 31-MAR-2000; 2000WO-US08802.
XX
XX 13-APR-1999; 99US-0291894.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Collins PL, Murphy BR, Whitehead SS;
PI
XX
XX WPI: 2000-679462/66.
DR
XX
XX Infectious chimeric respiratory syncytial virus (RSV) produced from
PT cloned nucleotide sequences, useful as a vaccine against diseases
PT caused by the virus, such as pneumonia and bronchiolitis -
PS
XX
XX Example 17; Fig 21; 280pp; English.
PS
XX
XX The present sequence represents a fusion of human respiratory
CC syncytial virus (RSV) NS1 gene 5' nontranslated region to the
CC NS2 coding region. PCR-mediated mutagenesis (see AAA88760-61) was
CC used to delete the NS1 gene coding region, 3' untranslated region,
CC the NS1-NS2 coding region and the NS2 5' nontranslated region, a
CC total of 529 nucleotides. The deleted region corresponds to
CC nucleotides 99-627 of the RSV antigenome cDNA given in AAA88743.
CC This type of deletion can be incorporated into viable recombinant
CC RSV of the invention to yield an altered phenotype, in this case
CC reduced rate of virus growth and reduced plaque size in vitro. The
CC invention relates to infectious chimeric RSV produced by introducing
CC 1 or more heterologous gene(s) or gene segment(s) from 1 RSV
CC subgroup or strain into a recipient RSV background of a different
CC subgroup or strain. The resulting chimeric RSV virus or subviral
CC particle is infectious and attenuated, preferably by introduction
CC of selected mutations. The chimeric RSV is useful as a vaccine
CC against RSV, which causes pneumonia and bronchiolitis in infants.
XX
SQ Sequence 33 BP; 12 A; 7 C; 6 G; 8 T; 0 other;
Query Match 48.7%; Score 14.6; DB 21; Length 33;
Best Local Similarity 81.0%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5 TCCTGGGTAGAGTGGGACAC 25
DB 9 TCCTGGGTAGAGTGGGACAC 29
```

Search completed: June 21, 2003, 22:26:18  
Job time : 167.531 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 ; Search time 35.625 Seconds  
(without alignments)  
258.254 Million cell updates/sec

Title: US-09-964-666-9

Perfect score: 30

Sequence: 1 TTCAATCTGGTAAAGAGTGGACACCTGTG 30

Scoring table:

IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 443362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*  
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3: /cgn2\_6/prodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	52.7	31	2	US-08-454-557C-63 Sequence 63, Appl
2	15.8	52.7	31	2	US-08-340-426D-63 Sequence 63, Appl
3	15.8	52.7	31	2	US-08-450-673C-63 Sequence 63, Appl
4	15.8	52.7	31	5	PCT-US95-1711A-63 Sequence 63, Appl
5	14.8	49.3	39	1	US-08-225-224-31 Sequence 31, Appl
6	14.8	49.3	39	3	US-08-722-258-31 Sequence 31, Appl
7	14.8	49.3	39	5	PCT-US95-04468-31 Sequence 31, Appl
8	14.8	49.3	42	1	US-08-225-224-28 Sequence 28, Appl
9	14.8	49.3	42	3	US-08-722-258-28 Sequence 28, Appl
10	14.8	49.3	42	5	PCT-US95-04468-28 Sequence 28, Appl
11	14.6	48.7	45	5	US-08-931-220-38 Sequence 38, Appl
12	14.6	48.7	45	5	PCT-US95-11723-38 Sequence 38, Appl
13	14.6	48.7	45	5	PCT-US96-05997-38 Sequence 38, Appl
14	14.2	47.3	20	4	US-09-742-703-12 Sequence 12, Appl
15	14.2	47.3	42	4	US-09-171-425-2 Sequence 2, Appl
16	14.2	47.3	48	4	US-09-171-425-6 Sequence 6, Appl
17	14.2	47.3	48	4	US-09-171-425-7 Sequence 7, Appl
18	14.2	47.3	48	4	US-07-977-434-38 Sequence 38, Appl
19	14.2	47.3	46	1	US-08-458-819-38 Sequence 38, Appl
20	14.2	47.3	46	5	PCT-US91-07035-38 Sequence 38, Appl
21	14.2	47.3	46	4	US-09-641-638-659 Sequence 659, App
22	13.8	46.0	26	4	US-08-859-998-1306 Sequence 1306, App
23	13.8	46.0	26	3	US-09-225-928-1306 Sequence 1306, App
24	13.8	46.0	36	3	US-08-041-953-5 Sequence 5, Appl
25	13.8	46.0	43	2	US-08-332-766A-5 Sequence 54, Appl
26	13.4	44.7	40	2	US-08-628-422-54 Sequence 60, Appl
27	13.4	44.7	40	4	US-09-306-998-60 Sequence 60, Appl

28	13.4	44.7	50	1	US-08-171-389-326 Sequence 326, App
29	13.4	44.7	50	1	US-08-123-936-326 Sequence 326, App
30	13.4	44.7	50	2	US-08-475-228A-326 Sequence 326, App
31	13.4	44.7	50	3	US-08-482-080A-326 Sequence 326, App
32	13.4	44.7	50	4	US-09-354-947-326 Sequence 326, App
33	13.4	44.7	50	5	PCT-US93-12388-326 Sequence 326, App
34	13.2	44.0	20	3	US-08-882-046-61 Sequence 61, Appl
35	13.2	44.0	26	1	US-08-621-914A-13 Sequence 13, Appl
36	13.2	44.0	33	1	US-08-244-626-30 Sequence 30, Appl
37	13.2	44.0	35	6	5256642-27 Patent No. 5256642
38	13.2	44.0	35	6	5472939-27 Patent No. 5472939
39	13.2	44.0	38	4	US-08-870-511-34 Sequence 34, Appl
40	13.2	44.0	39	1	US-08-469-486-33 Sequence 33, Appl
41	13.2	44.0	39	2	US-08-469-658-33 Sequence 33, Appl
42	13.2	44.0	42	6	5256642-28 Patent No. 5256642
43	13.2	44.0	42	6	5472939-28 Patent No. 5472939
44	13	43.3	24	5	PCT-US96-10905-23 Sequence 23, Appl
45	13	43.3	28	2	US-08-761-243C-25 Sequence 25, Appl

#### ALIGNMENTS

RESULT 1  
US-08-454-557C-63/C  
Sequence 63, Application US/08454557C  
Patent No. 5830670  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
APPLICANT: Mandis, Jack R.  
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
TITLE OF INVENTION: of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/454,557C  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ. ID NO.: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
US-08-454-557C-63  
Query Match 52.7%; Score 15.8; DB 2; Length 31;  
Best Local Similarity 74.1%; Pred. No. 93;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
OY 1 TTCAATCTGGTAAAGAGTGGACACCT 27  
DB 27 TTCAATCTGGTAAAGAGTGGACACCT 1

RESULT 2  
US-08-340-426D-63/C  
Sequence 63, Application US/08340426D  
Patent No. 5948634  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
TITLE OF INVENTION: of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,426D  
FILING DATE: 14-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
US-08-340-426D-63

Query Match 52.7%; Score 15.8; DB 2; Length 31;  
Best Local Similarity 74.1%; Pred. No. 93;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TTCATCCTGGTGAAGTGGACACCT 27  
||||| ||||| || ||||| |||  
Db 27 TTCAGCCTGGTGACAGACGAGATCT 1

RESULT 3  
US-08-450-673C-63/C  
Sequence 63, Application US/08450673C  
Patent No. 5948888  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
TITLE OF INVENTION: of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
US-08-450-673C-63

Query Match 52.7%; Score 15.8; DB 2; Length 31;  
Best Local Similarity 74.1%; Pred. No. 93;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TTCATCCTGGTGAAGTGGACACCT 27  
||||| ||||| || ||||| |||  
Db 27 TTCAGCCTGGTGACAGACGAGATCT 1

RESULT 4  
PCT-US95-17111A-63/C  
Sequence 63, Application PC/TUS9517111A  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and  
TITLE OF INVENTION: Detection of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17111A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/340,426  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
PCT-US95-17111A-63

Query Match 52.7%; Score 15.8; DB 5; Length 31;  
Best Local Similarity 74.1%; Pred. No. 93;  
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TTCATCCTGGTGAAGAGTGGACACCT 27  
|||||  
Db 27 TTCAGCCTGGGTGACGACGACGACATCT 1

RESULT 5  
US-08-225-224-31/c  
Sequence 31, Application US/08225224  
Patent No. 5635599  
GENERAL INFORMATION:  
APPLICANT: PASTAN, Ira  
APPLICANT: KREITMAN, Robert J.  
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,224  
FILING DATE: 8-APR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ. ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (primer)  
US-08-225-224-31

Query Match 49.3%; Score 14.8; DB 1; Length 39;  
Best Local Similarity 73.1%; Pred. No. 2.9e+02;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 2 TCATCTGGGTGAAGAGTGGACACCT 27  
|||||  
Db 26 TCACCGAGGTGAACGGTGGGACACT 1  
RESULT 6  
US-08-722-258-31/c  
Sequence 31, Application US/08722258  
Patent No. 6011002  
GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Kreitman, Robert J.  
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
TITLE OF INVENTION: CIRCULARLY PERMUTATED CHIMERIC MOLECULES  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California

COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/722,258  
FILING DATE: 08-JAN-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US95/04468  
FILING DATE: 06-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/225,224  
FILING DATE: 08-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-193100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ. ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY:  
LOCATION: 1..39  
OTHER INFORMATION: /note= "BK-138 primer"  
US-08-722-258-31

Query Match 49.3%; Score 14.8; DB 3; Length 39;  
Best Local Similarity 73.1%; Pred. No. 2.9e+02;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 2 TCATCCTGGGTGAAGAGTGGACACCT 27  
|||||  
Db 26 TCACCGAGGTGAACGGTGGGACACT 1  
RESULT 7  
PCT-US95-04468-31/c  
Sequence 31, Application PC/TUS9504468  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS  
NUMBER OF SEQUENCES: 59  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04468  
FILING DATE: 07-APR-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/225,224  
FILING DATE: 08-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-193-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (primer)  
PCT-US95-04468-31

Query Match 49.3%; Score 14.8; DB 5; Length 39;  
Best Local Similarity 73.1%; Pred. No. 2.9e+02;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TCATCCTGGGTAGAGTGGACACT 27  
||| | |||| | |||| | ||||  
Db 26 TCACCGAGGTACGCTGGGACACT 1

RESULT 8  
US-08-225-224-28  
Sequence 28, Application US/08225224  
Patent No. 5635599

GENERAL INFORMATION:  
APPLICANT: PASTAN, Ira  
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: Stewart Street Tower, One Market Plaza  
CITY: San Francisco  
STATE: California  
COUNTRY: US  
ZIP: 94105-1493

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,224  
FILING DATE: 8-APR-1994  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 13280-193  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (primer)  
US-08-225-224-28

Query Match 49.3%; Score 14.8; DB 1; Length 42;  
Best Local Similarity 73.1%; Pred. No. 2.9e+02;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TCATCCTGGGTAGAGTGGACACT 27  
||| | |||| | |||| | ||||  
Db 5 TCACCGAGGTACGCTGGGACACT 30

RESULT 9  
US-03-722-258-28  
Sequence 28, Application US/08722258  
Patent No. 6011002

GENERAL INFORMATION:  
APPLICANT: Pastan, Ira  
APPLICANT: Kreitman, Robert J.  
APPLICANT: Puri, Raj K.  
TITLE OF INVENTION: Circularly Permuted Ligands and  
TITLE OF INVENTION: Circularly Permuted Chimeric Molecules  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/722,258  
FILING DATE: 08-JAN-1997  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US95/04468  
FILING DATE: 06-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/225,224  
FILING DATE: 08-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 015280-193100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..42  
OTHER INFORMATION: /note= "BK-135 primer"

US-08-722-258-28

Query Match 49.3%; Score 14.8; DB 3; Length 42;  
Best Local Similarity 73.1%; Pred. No. 2.9e+02;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TCATCCTGGGTAGAGTGGACACT 27  
||| | |||| | |||| | ||||  
Db 5 TCACCGAGGTACGCTGGGACACT 30

RESULT 10  
PCT-US95-04468-28  
Sequence 28, Application PC/TUS9504468  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS  
NUMBER OF SEQUENCES: 59  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04468

FILED DATE: 07-APR-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/225,224  
FILING DATE: 08-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen L.  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 15280-193-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (primer)  
PCT-US95-04468-28

Query Match 49.3% Score 14.8; DB 5;  
Best Local Similarity 73.1%; Pred. No. 2.9e+02;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 TCATCTGGGTAAGAGTGGACACCT 27  
||| | |||| |||| |||| ||||  
Db 5 TCACCGAGGTAACGTCGGGACACCT 30

RESULT 11  
US-08-931-220-38/c  
Sequence 38, Application US/08931220  
Patent No. 6030835  
GENERAL INFORMATION:  
APPLICANT: Musser M.D., James M.  
APPLICANT: Kapur M.D., Vivek  
TITLE OF INVENTION: Methods and Compositions for Identifying  
TITLE OF INVENTION: Group A Streptococcus  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WEIL, GOTSHAL & MANCES  
STREET: 2882 Sand Hill Road, Suite 280  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025-7022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,220  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,542  
FILING DATE: 14-SEP-1994  
APPLICATION NUMBER: US 08/160,965  
FILING DATE: 02-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter Ph.D., Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: BAYL-004/01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 926-6200  
TELEFAX: (415) 854-3713  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
IMMEDIATE SOURCE:  
CLONE: speb19  
US-08-931-220-38

Query Match 48.7% Score 14.6; DB 3;  
Best Local Similarity 69.0%; Pred. No. 3.7e+02;  
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 TCATCTGGGTAAGAGTGGACACCTGTG 30  
||| | |||| |||| |||| ||||  
Db 33 TCATGTTGGGAAGGCGGGAACACTTTG 5

RESULT 12  
PCT-US95-11723-38/c  
Sequence 38, Application PC/TUS9511723  
GENERAL INFORMATION:  
APPLICANT: Musser M.D., James M.  
APPLICANT: Kapur M.D., Vivek  
TITLE OF INVENTION: Methods and Compositions for  
TITLE OF INVENTION: Identifying Streptococcus  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAW OFFICES OF BARBARA RAE-VENTER  
STREET: P.O. Box 60039  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/11723  
FILING DATE: 14-SEP-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,542  
FILING DATE: 14-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter Ph.D., Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: BAYL-004/03US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 926-6205  
TELEFAX: (415) 424-8760  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
IMMEDIATE SOURCE:  
CLONE: speb19  
PCT-US95-11723-38

Query Match 48.7% Score 14.6; DB 5;  
Best Local Similarity 69.0%; Pred. No. 3.7e+02;  
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 2 TCATCCTGGGTAAGAGTGGGACACTGTG 30  
1111 1111 1111 1111 1111  
Db 33 TCATGTTGGGAAGGGCGGACACTTTG 5

## RESULT 13

PCT-US96-05997-38/c  
Sequence 38, Application PC/TUS9605997  
GENERAL INFORMATION:  
APPLICANT: Musser M.D., James M.  
APPLICANT: Kapur M.D., Vivek  
APPLICANT: Ananthaswamy, H. N.  
APPLICANT: Fernandez, A.  
TITLE OF INVENTION: Use of extracellular cysteine protease  
TITLE OF INVENTION: to inhibit cell proliferation  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WEIL, GOTSIAL & MANGES  
STREET: 2882 Sand Hill Road, Suite 280  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025-7022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/05997  
FILING DATE: 01-MAY-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/306,542  
FILING DATE: 14-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,965  
FILING DATE: 02-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter Ph.D., Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: BAYL-004/0205  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 926-6200  
TELEFAX: (415) 854-3713  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
IMMEDIATE SOURCE:  
CLONE: speB19  
PCT-US96-05997-38

Query Match 48.7%; Score 14.6; DB 5; Length 45;  
Best Local Similarity 69.0%; Pred. No. 3.7e+02;  
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 2 TCATCCTGGGTAAGAGTGGGACACTGTG 30  
1111 1111 1111 1111 1111  
Db 33 TCATGTTGGGAAGGGCGGACACTTTG 5

RESULT 14  
US-09-742-703-12  
Sequence 12, Application US/09742703  
Patent No. 6423543

GENERAL INFORMATION:  
APPLICANT: Patrick Allen Marcotte  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF HEP5IN EXPRESSION  
FILE REFERENCE: RTS-0090  
CURRENT APPLICATION NUMBER: US/09/742,703  
CURRENT FILING DATE: 2000-12-20  
NUMBER OF SEQ ID NOS: 49  
SEQ ID NO 12  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-742-703-12

Query Match 47.3%; Score 14.2; DB 4; Length 20;  
Best Local Similarity 84.2%; Pred. No. 4.8e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 TCCTGGGTAAGAGTGGGAC 23  
11111111 11111111  
Db 2 TCCTGGGCCAGGAGTGGGAC 20

## RESULT 15

US-09-171-425-2  
Sequence 2, Application US/09171425A  
Patent No. 6465438  
GENERAL INFORMATION:  
APPLICANT: Schorf, Joachim  
APPLICANT: Baker, Henry J.  
APPLICANT: Smith, Bruce F.  
TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS  
FILE REFERENCE: 08909/003001  
CURRENT APPLICATION NUMBER: US/09/171,425A  
CURRENT FILING DATE: 1998-10-19  
EARLIER APPLICATION NUMBER: PCT/EP97/01943  
EARLIER FILING DATE: 1996-04-19  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 42  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated oligonucleotides  
US-09-171-425-2

Query Match 47.3%; Score 14.2; DB 4; Length 42;  
Best Local Similarity 70.4%; Pred. No. 5.6e+02;  
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 2 TCATCCTGGGTAAGAGTGGGACACTGTG 28  
1111 1111 1111 1111 1111  
Db 14 TCACCTGGCTAAGAGAAGAAAGACTG 40

Search completed: June 22, 2003, 00:01:29  
Job time : 38.625 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 22:26:37 ; Search time 88.5938 seconds  
(without alignments)  
496.907 Million cell updates/sec

Title: US-09-964-666-9

Perfect score: 30

Sequence: 1 TTCATCTCGGTAGAGTGGACCTGTG 30

Scoring table: IDENTITY NUC

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

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2: /cgn2\_6/ptodata/2/pubpna/PCCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

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9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

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11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*

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14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	9	US-09-964-667-9
2	30	100.0	30	10	US-09-964-666-9
3	30	100.0	30	10	US-09-964-412-9
4	22	73.3	22	9	US-09-964-667-5
5	22	73.3	22	10	US-09-964-666-5
6	22	73.3	22	10	US-09-964-412-5
7	15.6	52.0	25	9	US-10-098-263B-65996
8	15.2	50.7	45	10	US-09-965-602-27
9	15	50.0	43	9	US-09-802-640-9
10	14.8	49.3	30	9	US-10-085-906-97
11	14.8	49.3	31	10	US-09-801-274-8
12	14.6	48.7	25	9	US-10-215-112-7585
13	14.6	48.7	25	9	US-10-215-112-12152
14	14.6	48.7	25	9	US-10-098-263B-97774
15	14.6	48.7	25	9	US-10-098-263B-129375
16	14.4	48.0	49	9	US-09-860-670-233
17	14.2	47.3	25	9	US-10-098-263B-3274
18	14.2	47.3	36	9	US-10-294-778-8
19	14.2	47.3	39	9	US-10-011-672-9

20	14.2	47.3	39	9	US-10-012-013-9	Sequence 9, Appl
21	14.2	47.3	39	9	US-10-012-070A-9	Sequence 9, Appl
22	14	46.7	25	9	US-10-098-263B-44679	Sequence 44679, A
23	14	46.7	25	9	US-10-098-263B-65995	Sequence 65995, A
24	14	46.7	31	9	US-09-912-263-86	Sequence 86, Appl
25	13.8	46.0	31	10	US-09-801-274-873	Sequence 873, App
26	13.6	45.3	25	9	US-10-060-895A-1142	Sequence 1142, Ap
27	13.6	45.3	25	9	US-10-060-895A-1143	Sequence 1143, Ap
28	13.6	45.3	25	9	US-10-060-895A-1144	Sequence 1144, Ap
29	13.6	45.3	25	9	US-10-060-895A-1145	Sequence 1145, Ap
30	13.6	45.3	25	9	US-10-060-895A-1146	Sequence 1146, Ap
31	13.6	45.3	25	9	US-10-060-895A-1147	Sequence 1147, Ap
32	13.6	45.3	25	9	US-10-060-895A-1148	Sequence 1148, A
33	13.6	45.3	25	9	US-10-098-263B-103293	Sequence 103293, A
34	13.4	44.7	25	9	US-10-098-263B-26559	Sequence 26559, A
35	13.4	44.7	25	9	US-10-098-263B-26737	Sequence 26737, A
36	13.4	44.7	25	9	US-10-098-263B-103293	Sequence 103293, A
37	13.4	44.7	25	9	US-10-098-263B-125737	Sequence 125737, A
38	13.4	44.7	30	9	US-10-082-772-9	Sequence 9, Appl
39	13.4	44.7	31	9	US-09-864-636A-2477	Sequence 2477, Ap
40	13.4	44.7	40	9	US-09-951-402-60	Sequence 60, Appl
41	13.4	44.7	40	10	US-09-922-101-60	Sequence 60, Appl
42	13.4	44.7	25	9	US-10-060-895A-1148	Sequence 1148, Ap
43	13.2	44.0	25	9	US-10-060-895A-1149	Sequence 1149, Ap
44	13.2	44.0	25	9	US-10-098-263B-19558	Sequence 19558, A
45	13.2	44.0	25	9		

## ALIGNMENTS

RESULT 1

US-09-964-667-9

Sequence 9, Application US/09964667

Publication No. US20030033621A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Wands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,667

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-964-667-9

Query Match 100.0%; Score 30; DB 9; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCATCCTGGTAAAGAGTGGGACACCTGTG 30

DB 1 TTTCATCCTGGTAAAGAGTGGGACACCTGTG 30

RESULT 2

US-09-964-666-9

Sequence 9, Application US/09964666

Patent No. US20020104108A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESS: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-964-666-9

Query Match

Best Local Similarity 100.0%; Score 30; DB 10; Length 30;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCATCCTGGTAAAGAGTGGGACACCTGTG 30

DB 1 TTTCATCCTGGTAAAGAGTGGGACACCTGTG 30

RESULT 3

US-09-964-412-9

Sequence 9, Application US/09964412

Patent No. US20020129391A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESS: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-964-412-9

Query Match

Best Local Similarity 100.0%; Score 30; DB 10; Length 30;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCATCCTGGTAAAGAGTGGGACACCTGTG 30

DB 1 TTTCATCCTGGTAAAGAGTGGGACACCTGTG 30

RESULT 4

US-09-964-667-5/C

Sequence 5, Application US/09964667

Publication No. US2003003621A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESS: Sterne, Kessler, Goldstein &amp; Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,667

FILING DATE: 28-Sep-2001

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.



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1  REGISTRATION NUMBER: 32,893
2  REFERENCE/DOCKET NUMBER: 0609.4370000
3  TELECOMMUNICATION INFORMATION:
4  TELEPHONE: 202-371-2600
5  TELEFAX: 202-371-2540
6  INFORMATION FOR SEQ ID NO: 5:
7  SEQUENCE CHARACTERISTICS:
8  LENGTH: 22 base pairs
9  TYPE: nucleic acid
10 STRANDEDNESS: single
11 TOPOLOGY: linear
12 MOLECULE TYPE: cDNA
13 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
14
15 US-09-964-667-5
16
17 Query Match 73.3%; Score 22; DB 9; Length 22;
18 Best Local Similarity 100.0%; Pred. No. 0.74;
19 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
20
21 3 CATCCTGGTAGAGTGGGACA 24
22 CATCCTGGTAGAGTGGGACA 1
23
24 RESULT 5
25 US-09-964-666-5/c
26 Sequence 5, Application US/09964666
27 Patent No. US20020104108A1
28 GENERAL INFORMATION:
29 APPLICANT: de la Monte, Suzanne
30 Mands, Jack R.
31 TITLE OF INVENTION: Transgenic Animals and Cell Lines for
32 Screening Drugs Effective for the Treatment or Prevention
33 of Alzheimer's Disease
34 NUMBER OF SEQUENCES: 14
35 CORRESPONDENCE ADDRESS:
36 ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
37 STREET: 1100 New York Ave., Suite 600
38 CITY: Washington
39 STATE: DC
40 COUNTRY: USA
41 ZIP: 20005-3934
42 COMPUTER READABLE FORM:
43 MEDIUM TYPE: Floppy disk
44 COMPUTER: IBM PC compatible
45 OPERATING SYSTEM: PC-DOS/MS-DOS
46 SOFTWARE: PatentIn Release #1.0, Version #1.30
47 CURRENT APPLICATION DATA:
48 APPLICATION NUMBER: US/09/964,666
49 FILING DATE: 28-Sep-2001
50 CLASSIFICATION: <Unknown>
51 ATTORNEY/AGENT INFORMATION:
52 NAME: Esmond, Robert W.
53 REGISTRATION NUMBER: 32,893
54 REFERENCE/DOCKET NUMBER: 0609.4370000
55 TELECOMMUNICATION INFORMATION:
56 TELEPHONE: 202-371-2540
57 TELEFAX: 202-371-2600
58 INFORMATION FOR SEQ ID NO: 5:
59 SEQUENCE CHARACTERISTICS:
60 LENGTH: 22 base pairs
61 TYPE: nucleic acid
62 STRANDEDNESS: single
63 TOPOLOGY: linear
64 MOLECULE TYPE: cDNA
65 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
66
67 US-09-964-666-5
68
69 Query Match 73.3%; Score 22; DB 10; Length 22;
70 Best Local Similarity 100.0%; Pred. No. 0.74;
71 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
72
73 3 CATCCTGGTAGAGTGGGACA 24

```

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Db          22 CATCTGGGTAGAGTGGGACA 1
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RESULT 6
US-09-964-412-5/c
Sequence 5, Application US/09964412
Patent No. US20020129391A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
Wands, Jack R.
TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/964,412
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609,4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-964-412-5
Query Match 73.3%, Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          3 CATCTGGGTAGAGTGGGACA 24
|||||
Db          22 CATCTGGGTAGAGTGGGACA 1
|||||
RESULT 7
US-10-098-263B-65996
Sequence 65996, Application US/10098263B
Publication No. US2003010410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 65996
LENGTH: 25

```

TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-098-263B-65996

Query Match 52.0%; Score 15.6; DB 9; Length 25;  
Best Local Similarity 81.8%; Pred. No. 6.9e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 TCCTGGGTAGAGTGGACACC 26  
||| ||| ||| ||| ||| ||| |||  
DB 3 TCCTGGGTAGAGTGGACACC 24

RESULT 8  
US-09-965-602-27/c  
Sequence 27, Application US/09965602  
Patent No. US20020103154A1  
GENERAL INFORMATION:  
APPLICANT: Dimster-Deak, Dago  
TITLE OF INVENTION: ESSENTIAL GENES IN YEAST AS TARGETS FOR ANTIFUNGAL  
TITLE OF INVENTION: AGENTS,  
FILE REFERENCE: HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION DRUGS  
CURRENT FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: US/09/539,697  
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 27  
LENGTH: 45  
TYPE: DNA  
ORGANISM: primer  
US-09-965-602-27

Query Match 50.7%; Score 15.2; DB 10; Length 45;  
Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CATCTGGGTAGAGTGGGA 22  
||| ||| ||| ||| ||| ||| |||  
DB 45 CATCTGGGTAGAGTGGGA 26

RESULT 9  
US-09-802-640-9/c  
Sequence 9, Application US/09802640  
Publication No. US20030036057A1  
GENERAL INFORMATION:  
APPLICANT: Braun, Andreas  
APPLICANT: Bonsal Aruna  
APPLICANT: Kleya Patrick  
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: 24736-2048  
CURRENT APPLICATION NUMBER: US/09/802,640  
CURRENT FILING DATE: 2001-03-09  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 43  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PCR primer  
US-09-802-640-9

Query Match 50.0%; Score 15; DB 9; Length 43;  
Best Local Similarity 78.3%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 8 TGGTAAGAGTGGACACCTGTG 30  
| |||| | |||| |||| |||| ||||

DB 40 TAGTAGGCGGTGTCACCTGTG 18

RESULT 10  
US-10-085-906-97  
Sequence 97, Application US/10085906  
Publication No. US20030054371A1  
GENERAL INFORMATION:  
APPLICANT: Vlug, Vincent  
APPLICANT: Wu, Paul  
APPLICANT: Gray, Gary S.  
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
FILE REFERENCE: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF  
FILE REFERENCE: GNN-5343CP2  
CURRENT APPLICATION NUMBER: US/10/085,906  
CURRENT FILING DATE: 2002-02-27  
PRIOR APPLICATION NUMBER: US 60/126,215  
PRIOR FILING DATE: 1999-03-25  
PRIOR APPLICATION NUMBER: US 09/534,061  
PRIOR FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: PCT/US00/07938  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 545  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 97  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-085-906-97

Query Match 49.3%; Score 14.8; DB 9; Length 30;  
Best Local Similarity 73.1%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TTCATCTGCGTAAAGTGGACACC 26  
| |||| |||| | || |||| ||  
DB 1 TCATCTGCGGCGACAGAGACATCC 26

RESULT 11  
US-09-801-274-8  
Sequence 8, Application US/09801274  
Patent No. US20020032319A1  
GENERAL INFORMATION:  
APPLICANT: Carvill, Michele  
APPLICANT: Ireland, James S.  
APPLICANT: Lander, Eric S.  
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS  
FILE REFERENCE: 2825.2009-001  
CURRENT APPLICATION NUMBER: US/09/801,274  
CURRENT FILING DATE: 2001-03-07  
PRIOR APPLICATION NUMBER: US 60/187,510  
PRIOR FILING DATE: 2000-03-07  
PRIOR APPLICATION NUMBER: US 60/206,129  
PRIOR FILING DATE: 2000-05-22  
NUMBER OF SEQ ID NOS: 1802  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 31  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-801-274-8

Query Match 49.3%; Score 14.8; DB 10; Length 31;  
Best Local Similarity 67.9%; Pred. No. 1.6e+03;  
Matches 19; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 3 CATCTGGGTAGAGTGGACACCTGTG 30  
||| ||| | || |||| |||| ||  
DB 2 CATCAAGGATGATGATGACACCTGCC 29

RESULT 12

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US-10-215-112-7585
; Sequence 7585, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7585
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-7585

Query Match
Best Local Similarity 48.7%; Score 14.6; DB 9; Length 25;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTGGTAAGAGTGGGACACCT 27
Db 2 CTAGGAAGGTTGGGACACCT 22

RESULT 13
US-10-215-112-12152/c
; Sequence 12152, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12152
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12152

Query Match
Best Local Similarity 48.7%; Score 14.6; DB 9; Length 25;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTGGTAAGAGTGGGACACCT 27
Db 24 CTAGGAAGGTTGGGACACCT 4

RESULT 14
US-10-098-263B-97774/c
; Sequence 97774, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 97774
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-97774

Query Match
Best Local Similarity 48.7%; Score 14.6; DB 9; Length 25;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 TGGGTAAGAGTGGGACACCTG 28
Db 23 TGTGTAAGAGTGGTACCACCTG 3

RESULT 15
US-10-098-263B-129375/c
; Sequence 129375, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 129375
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-129375

Query Match
Best Local Similarity 48.7%; Score 14.6; DB 9; Length 25;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TCCTGGGTAAGAGTGGGACAC 25
Db 25 TCCTGGGTCGAGTGTACAC 5
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Search completed: June 22, 2003, 03:18:14  
Job time : 96.5938 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:28:37 ; Search time 1295.86 seconds  
(without alignments)  
374.936 Million cell updates/sec

Title: US-09-964-666-9

Perfect score: 30

Sequence: 1 TTCATCTGCTGAGAGTGGACACCTGTG 30

Scoring table: Identity\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estlin:*
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5: em_estcov:*
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7: em_estro:*
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9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
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13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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17: gb_gss:*
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19: em_gss_inv:*
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22: em_gss_fun:*
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24: em_gss_mus:*
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26: em_gss_pro:*
27: em_gss_trod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16.6	55.3	48	14	H39590 ypo107.r1
C 2	16.4	54.7	50	9	AU102898 AU102898
C 3	16.4	54.7	50	9	AU106860 AU106860
C 4	16.2	54.0	48	17	A2796512 A2796512
C 5	16	53.3	50	9	AU106864 AU106864
C 6	15.4	51.3	46	9	AI439612 AI439612

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	COMMENT
H39590/c			H39590							
48 bp	MRNA	linear	EST 16-AUG-1995							
yp0107.r1	Soares breast 3NDBST Homo sapiens cDNA clone									
IMAGE:186204 5'	similar to gb U87904 HUMALNE531 Human carcinoma									
cell-derived Alu RNA transcript. (cRNA):	gb U81695 LEUCOCYTE									
ADHESION GLYCOPROTEIN P150,95 ALPHA CHAIN (HUMAN);	MRNA sequence.									
H39590										
H39590.1	GI:915642									
EST.										
human.										
Homo sapiens										
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;										
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.										
1 (bases 1 to 48)										
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,										
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,										
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Treviskis, F., Waterston,										
R., Williamson, A., Wohlmann, P., and Wilson, R.										
The Wasnu-Merck EST Project										
Unpublished (1995)										
Contact: Wilson RK										
Washington University School of Medicine										
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108										
Tel: 314 286 1800										
Fax: 314 286 1810										
Email: estw@wustl.edu										
Insert Size: 730										
High quality sequence starts: 1										

#### ALIGNMENTS

1024893	0U52B04.x	1024893	0U52B04.x
R08290	yf18e09.s1		
N38850	yy80e11.s1		
A2575761	AST-r32B0		
AU258691	AU258691		
AU108052	AU108052		
A1900587	sc13c051.y		
AA871520	vg36e071.r		
H99413	yk24f02.s1		
T96362	ye49c04.s1		
AU104029	AU104029		
AU107906	AU107906		
AV951566	AV951566		
AL737914	Danio fer		
AI697225	tq17d081.x		
AU103750	AU103750		
B1522018	603081709		
D11989	HUM0005134		
H39150	yn83e09.r1		
H84235	ys65f06.s1		
AA976917	gc35h041.s		
H14824	ym25d07.s1		
AA410762	zc35e11.r		
C20874	HUMGS000494		
C20875	HUMGS000494		
D12406	HUM00TW129		
A2576739	AST-2T007		
AA934082	on27q11.s		
AA928240	on87c07.s		
AU102621	AU102621		
H41620	y009b09.r1		
T78935	yd21f08.s1		
N80349	za13c12.r1		
A1801185	to79n04.x		
A1900587	sc13c051.y		
A1494250	gy98a01.x		
AU104332	AU104332		
A2373047	1M0125j11		
A1620509	tu56f04.x		

High quality sequence stops: 1  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Insert length: 730 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 1.

BASE	COUNT			
a	8	c	10	g
t	14	others	3	

Query Match	55.3%	Score 16.6	DB 14	Length 48
Best Local Similarity	76.0%	Pred. No. 7.9e+03		
Matches 19, Conservative	0	Mismatches 6	Indels 0	Gaps 0

RESULT	2
AU102898/c	
LOCUS	
DEFINITION	50 bp mRNA library Homo sapiens CDNA clone
ACCESSION	AU102898 Sugano Homo sapiens CDNA sequence.
VERSION	AU102898.1 GI:13552419
KEYWORDS	EST.
SOURCE	human.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Mammalia; Eumetaria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tanoda,T., Mizushima-Sugano,J., Sese,J., Hatake,  
H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakai,  
Y., Nakamura,Y., Suyama,A. and Sugano,S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001).

JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE	21270072
COMMENT	Contact: Yutaka Suzuki

FEATURES	Location/Qualifiers
source	1, .50

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/clone_lib="Sugano Homo sapiens cDNA library"
/notes="differential display comparison of untreated and
dimechyl fumarate treated u937 cells"

BASE COUNT      9 a      12 c      16 g      13 t
ORIGIN

Query Match      54.7%;      Score 16.4;      DB 9;      Length 50;
Best Local Similarity 76.9%;      Pred. No. 9.66+03;
Matches 20;      Conservative 0;      Mismatches 6;      Indels 0;      Gaps

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	Query Match	54.7%	Score 16.4	DB 9	Length 50
	Best Local Similarity	76.9%	Pred. No. 9,6e+03		
	Matches	20	Conservative	0	Mismatches 6, Indels 0, Gaps 0
Q7	1	TTCATCCGCGGTAAAGATGGGACACC	26		
	1				
	1				
	1				
Db	35	TTCACGCTCGGTGACAGAGGAGACCC	10		

RESULT 3	LOCUS	DEFINITION	ACCESSION	VERSION *	KEYWORDS	SOURCE	ORGANISM
AU106860/c	AU106860	50 bp mRNA	AU106860			human	Homo sapiens
	AU106860	Sugano Homo sapiens CDNA library	COJ03340				
	AU106860	mRNA sequence.	AU106860				
	AU106860.1	GI:13556381					
	EST.						
	linear	EST 30-AUG-2001					
		Homo sapiens CDNA clone					

REFERENCE	1 (bases 1 to 50)
AUTHORS	Suzuki, Y., Taira, H., Tsunoda, T., Minushima-Sugano, J., Sese, J., H. Y., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakakura, Y., Nakamura, Y., Sugiyama, A. and Sugano, S.
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE	21270072
COMMENT	Contact: Yutaka Suzuki

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. *Gene* 200 (1-2), 149-156 (1997).

Location/Qualifiers  
1..50

FEATURES

source

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/clone.lib="Sugano Homo sapiens cDNA library"
/notes="differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT      7 a      10 c      11 g      22 t
ORIGIN

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Db		49	TTCAGCCTGGCTGCACAGAGAGACC	24

LOCUS	A2796512	48 bp	DNA	' linear	GSS 16-FEB-2001
DEFINITION	ZM0052H18F Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C2M0052H18 F, DNA sequence.				
ACCESSION	A2796512				
VERSION	A2796512.1	GI:12944647			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				

ACCESSION	A2796512
VERSION	A2796512.1
KEYWORDS	GI:12944647
SOURCE	GSS.
ORGANISM	house mouse. <i>Mus musculus</i>

ACCESSION	A2796512
VERSION	A2796512.1
KEYWORDS	GI:12944647
SOURCE	GSS.
ORGANISM	house mouse. <i>Mus musculus</i>

REFERENCE 1 (bases 1 to 48)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mamoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10Kb plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0052 row: H column: 18  
 Seq primer: CGTTGTAACGACGCCAGT  
 Class: Plasmid ends  
 High quality sequence stop: 48.  
 FEATURES  
 source  
 1. 48  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCG2M0052H18"  
 /clone\_lib="Mouse 10Kb plasmid UUCGM library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g147321419b/AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
 BASE COUNT  
 8 a 10 c 15 g 15 t  
 ORIGIN  
 Query Match 54.0%; Score 16.2; DB 17; Length 48;  
 Best Local Similarity 72.4%; Pred. No. 1.1e+04;  
 Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 2 TCATCTGGGTAAAGTGGGACACCTGTG 30  
 Db 12 TCTTGTGGGTACATCTGGGACACATGTG 40  
 RESULT 5  
 AUI06864/c 50 bp mRNA linear EST 30-AUG-2001  
 LOCUS AUI06864 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 DEFINITION NBLAN21NRL1 mRNA sequence.  
 ACCESSION AUI06864  
 VERSION AUI06864.1 GI:13556385  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)  
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.  
 TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 MEDLINE 21270072  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@iems.u-tokyo.ac.jp  
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S.  
 TITLE Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  
 FEATURES  
 source  
 1. 50  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="NBLAN21NRL1"  
 /clone\_lib="Sugano Homo sapiens cDNA library"  
 /note="Differential display comparison of untreated and dimethylsulphate-treated U937 cells"  
 BASE COUNT  
 10 a 14 c 15 g 11 t  
 ORIGIN  
 Query Match 53.3%; Score 16; DB 9; Length 50;  
 Best Local Similarity 79.2%; Pred. No. 1.4e+04;  
 Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 CATCTGGGTAAAGTGGGACACCC 26  
 Db 28 CAGCCTGGGTGACAGAGGAGACC 5  
 RESULT 6  
 A1439612 46 bp mRNA linear EST 28-MAR-1999  
 LOCUS tc91b01.x1 NCI-CGAP-CL1 Homo sapiens cDNA clone IMAGE:2073481 3  
 DEFINITION similar to gb:U35531 GALACTOSIDE 2-L-FUCOSYLTRANSFERASE (HUMAN);, mRNA sequence.  
 ACCESSION A1439612  
 VERSION A1439612.1 GI:4305543  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 46)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps@remail.nih.gov  
 Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html  
 Trace considered overall poor quality  
 Insert length: 1378 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 46  
 source

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:2073481"  
/clone\_lib="NCI\_CGAP\_CLL1"  
/tissue\_type="B-cell, chronic lymphocytic leukemia"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5].  
TCTTACCATCTGTAAGTGGAGGCGCCGCTTTTCTTTTCTTTTCTTTT  
T 3'; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT  
ORIGIN  
18 a 10 c 11 g 7 t

Query Match  
Best Local Similarity 51.3%; Score 15.4; DB 9; Length 46;  
76.0%; Pred. No. 2.3e+04;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY  
1 TTCATCTGGGTAGTGGGACAC 25  
1 11111111111111111111  
1 TCCAGCTGGGCAACAGAGGACAC 25

Db  
1 TTCATCTGGGTAGTGGGACAC 25  
1 11111111111111111111  
1 TCCAGCTGGGCAACAGAGGACAC 25

RESULT 7  
AI024893 50 bp mRNA linear EST 27-AUG-1998  
LOCUS  
DEFINITION  
O525204.x1 NCI\_CGAP-Br2 Homo sapiens cDNA clone IMAGE:1631407 3'  
similar to contains Alu repetitive element; mRNA sequence.  
AI024893  
AI024893.1 GI:3240506  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www.bio.lim.gov/db/ftp/image/image.html  
Insert length: 305 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham.  
Location/Qualifiers  
1. 50  
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/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:1631407"  
/clone\_lib="NCI\_CGAP\_Br2"  
/sex="female, pooled"  
/tissue\_type="breast"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker. 1st strand cDNA was prepared from pooled bulk  
breast tumor tissue, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified pT73  
vector. This library is the normalized version of  
NCI\_CGAP\_Br1.1. Library was constructed by Bento Soares

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:2073481"  
/clone\_lib="NCI\_CGAP\_CLL1"  
/tissue\_type="B-cell, chronic lymphocytic leukemia"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5].  
TCTTACCATCTGTAAGTGGAGGCGCCGCTTTTCTTTTCTTTTCTTTT  
T 3'; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT  
ORIGIN  
12 a 11 c 12 g 15 t

Query Match  
Best Local Similarity 51.3%; Score 15.4; DB 9; Length 50;  
76.0%; Pred. No. 2.4e+04;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY  
3 CATCTGGGTAGTGGGACACCT 27  
1 11111111111111111111  
43 CACCTGGGTAGTGGGACACCT 19

Db  
3 CATCTGGGTAGTGGGACACCT 27  
1 11111111111111111111  
43 CACCTGGGTAGTGGGACACCT 19

RESULT 8  
R08290 47 bp mRNA linear EST 05-APR-1995  
LOCUS  
DEFINITION  
Y118609.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
IMAGE:127240 3' similar to gb|U87933|HUMALU364 Human carcinoma  
cell-derived Alu RNA transcript, (rRNA); mRNA sequence.  
R08290  
R08290.1 GI:760213  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 47)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston  
, R., Williamson, A., Wohlmann, P., and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson R.  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 716  
High quality sequence starts: 1 High quality sequence stops: 1  
Source: IMAGE Consortium, LINL This clone is available royalty-free  
through LINL; contact the IMAGE Consortium (info@image.lim.gov)  
for further information. Trace considered overall poor quality  
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Seq primer: -21ml3  
High quality sequence stop: 1.  
Location/Qualifiers  
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/db\_xref="GDB:479401"  
/db\_xref="taxon:9606"  
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/sex="male"  
/dev\_stage="20 week post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)  
with a modified polylinker. Site 1: Pac I; Site 2: Eco RI;  
1st strand cDNA was primed with a Pac I - oligo(dT) primer  
[5]. AACGTGACAGATTAATTAACATCTTTTCTTTTCTTTTCTTTT 3';  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
ORIGIN  
11 a 13 c 10 g 10 t

Query Match  
Best Local Similarity 50.0%; Score 15; DB 14; Length 47;  
72.0%; Pred. No. 3.4e+04;  
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;





REFERENCE 1 (bases 1 to 48)  
 AUTHORS Kato, K. and Matoba, R.  
 TITLE Generation of expressed sequence tags from mouse brain  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kikuya Kato  
 Graduate School of Biological Sciences  
 Nara Institute of Science and Technology  
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
 Tel: 81-743-72-5581  
 Fax: 81-743-72-5589  
 Email: kkatobds.aist-nara.ac.jp,  
 URL: http://love2.aist-nara.ac.jp/bed/index.html.

## FEATURES

source

1. 48

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone="BED0013497"

/clone\_lib="3'-directed mouse cDNA library"

/tissue\_type="brain"

/note="Vector: pGEM-T-easy"

Location/Qualifiers

15 a 15 c 7 g 10 t 1 others

BASE COUNT

15 a 15 c 7 g 10 t 1 others

ORIGIN

Query Match 49.3%; Score 14.8; DB 9; Length 48;  
 Best Local Similarity 70.4%; Pred. No. 4.1e+04;  
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

3 CATCCGGGTAGAGTGACACCTGT 29  
 12 CATCGCTGCTACACAGTGAANCGT 38

Db

RESULT 12  
 LOCUS AU108052 50 bp mRNA linear EST 30-AUG-2001  
 DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

ACCESSION AU108052  
 VERSION AU108052  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)  
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Oka, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.  
 TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
 source  
 1. 50  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="COLE0015"  
 /clone\_lib="Sugano Homo sapiens cDNA library"  
 /note="Differential display comparison of untreated and dimethylformate treated U937 cells"

BASE COUNT 8 a 11 c 17 g 14 t  
 ORIGIN

Query Match 49.3%; Score 14.8; DB 9; Length 50;

Best Local Similarity 73.1%; Pred. No. 4.2e+04;  
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

1 TTCATCTGCTAGAGTGGACACC 26  
 36 TCCAGCTGCTGACACAGCAGACC 11

Db

RESULT 13  
 LOCUS AI900587 40 bp mRNA linear EST 30-NOV-2001  
 DEFINITION sc13c05.y1 Gm-c1013 glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
 Gm-c1013-513 5' similar to TR:064621 064621 HYPOTHETICAL 82.1 KD  
 PROTEIN. ; mRNA sequence.

ACCESSION AI900587  
 VERSION AI900587  
 KEYWORDS EST.  
 SOURCE soybean.  
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 40)  
 AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Smaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
 TITLE Public Soybean EST Project  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Shoemaker R/Public Soybean EST Project  
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Trace considered overall poor quality  
 Possible reversed clone: similarity on wrong strand This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800) 533-4363 or contact via email: ccutresgen.com  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 40  
 /organism="Glycine max"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1013-513"  
 /clone\_lib="Gm-c1013"  
 /tissue\_type="whole seedlings, 2-3 week old seedlings, greenhouse grown"  
 /lab\_host="XL10-Gold"  
 /note="Vector: pBluescript II XR; site: 1: EcoRI; site: 2: XhoI; This cDNA library was constructed from mRNA isolated from whole seedlings of 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

BASE COUNT 10 a 7 c 17 g 6 t  
 ORIGIN

Query Match 48.7%; Score 14.6; DB 9; Length 40;



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